



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Suzuki, Shintaro

(ii) TITLE OF INVENTION: Protocadherin Materials and Methods

(iii) NUMBER OF SEQUENCES: 115

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA
(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent In Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 18 JUN 1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/263,161
(B) FILING DATE: 27 JUN 1994

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AARSSNNNTNG AYTRYGA

17

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTRCTRTTTC GNGGNNN

17

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGGGAGTGG ACTTTGAGGA GCAGCCTGAG CTTAGTCTCA TCCTCACGGC TTTGGATGGA	60
GGGACTCCAT CCAGGTCTGG GACTGCATTG GTTCAAGTGG AAGTCATAGA TGCCAATGAC	120
AACGCACCGT A	131

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Gly Val Asp Phe Glu Glu Gln Pro Glu Leu Ser Leu Ile Leu Thr	
1 5 10 15	
Ala Leu Asp Gly Gly Thr Pro Ser Arg Ser Gly Thr Ala Leu Val Gln	
20 25 30	
Val Glu Val Ile Asp Ala Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAACGCATGG ATTTCGAGGA GTCTTCCTCC TACCAAGATCT ATGTGCAAGC TACTGACCGG	60
GGACCAGTAC CCATGGCGGG TCATTGCAAG GTGTTGGTGG ACATTATAGA TGTGAACGAC	120
AACGCACCTA A	131

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Ala Met Asp Phe Glu Glu Ser Ser Ser Tyr Gln Ile Tyr Val Gln	
1 5 10 15	
Ala Thr Asp Arg Gly Pro Val Pro Met Ala Gly His Cys Lys Val Leu	
20 25 30	
Val Asp Ile Ile Asp Val Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCGACTGG ACTTTGAGAC CCTGCAGACC TTTCGAGTTCA GCGTGGGTGC CACAGACCAT	60
GGCTCCCCCT CGCTCCGCAG TCAGGCTCTG GTGCGCGTGG TGGTGCTGGA CCACAATGAC	120
AATGCCCA A	131

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Arg Leu Asp Phe Glu Thr Leu Gln Thr Phe Glu Phe Ser Val Gly
1 5 10 15

Ala Thr Asp His Gly Ser Pro Ser Leu Arg Ser Gln Ala Leu Val Arg
20 25 30

Val Val Val Leu Asp His Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGGGCCTGG ATTACGAGGC ACTGCAGTCC TTTCGAGTTCT ACGTGGGCGC TACAGATGGA 60

GGCTCACCCG CGCTCAGCAG CCAGACTCTG GTGCGGATGG TGGTGCTGGA TGACAACGAC 120

AACGCCCTA A 131

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Gly Leu Asp Tyr Glu Ala Leu Gln Ser Phe Glu Phe Tyr Val Gly
1 5 10 15

Ala Thr Asp Gly Gly Ser Pro Ala Leu Ser Ser Gln Thr Leu Val Arg
20 25 30

Met Val Val Leu Asp Asp Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGGCGTTG ATTTGAGGAG TCAGAGAGAG TTCCAGCTAA CCGCTCATAT AAACGACGGA 60
GGTACCCCGG TTTTGGCCAC CAACATCAGC GTGAACATAT TTGTTACTGA CCGCAATGAC 120
AACGCCCGC A 131

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys Ala Phe Asp Phe Glu Asp Gln Arg Glu Phe Gln Leu Thr Ala His
1 5 10 15

Ile Asn Asp Gly Gly Thr Pro Val Leu Ala Thr Asn Ile Ser Val Asn
20 25 30

Ile Phe Val Thr Asp Arg Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAGGCCGTGG ATTACGAAAT CACCAAGTCC TATGAGATAG ATGTTCAAGC CCAAGATCTG	60
GGTCCAATT CTATTCCCTGC TCATTGAAA ATTATAATTA AGGTCGTGGA TGTCAACGAC	120
AACGCTCCCA A	131

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Ala Val Asp Tyr Glu Ile Thr Lys Ser Tyr Glu Ile Asp Val Gln	
1 5 10 15	
Ala Gln Asp Leu Gly Pro Asn Ser Ile Pro Ala His Cys Lys Ile Ile	
20 25 30	
Ile Lys Val Val Asp Val Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TATGACCATG ATTACGAGAC AACCAAAGAA TATACACTGC GGATCCGGGC CCAGGGATGGT	60
GGCCGGACTC CACTTTCATA CGTCTCCGGT CTAGTAACCG TGCAGGTCTT AGACATCAAC	120
GACAATGCC CCCCC	135

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Tyr Asp His Asp Tyr Glu Thr Thr Lys Glu Tyr Thr Leu Arg Ile Arg
1 5 10 15

Ala Gln Asp Gly Gly Arg Thr Pro Leu Ser Asn Val Ser Gly Leu Val
20 25 30

Thr Val Gln Val Leu Asp Ile Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGGGGTCGA TTACGAGGAG AACGGCATGT TAGAGATCGA CGTGCAGGCC AGAGACCTAG 60

GACCTAACCC AATTCCAGCC CATTGCAAGG TCACAGTCAA GCTCATCGAC CGCAATGATA 120

ACGCCCCCA 129

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Gly Val Asp Tyr Glu Glu Asn Gly Met Leu Glu Ile Asp Val Gln
1 5 10 15

Ala Arg Asp Leu Gly Pro Asn Pro Ile Pro Ala His Cys Lys Val Thr
20 25 30

Val Lys Leu Ile Asp Arg Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAGGGGTTGG ACTACGAAGA CACCAAATC CATGAGATTT ACATCCAGGC CAAAGACAAA	60
GGTGCCAATC CGGAAGGAGC GCATTGCAAA GTACTGGTAG AGGTTGTGGA CGTTAACGAC	120
AATGCCCTC A	131

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys	Gly	Leu	Asp	Tyr	Glu	Asp	Thr	Lys	Leu	His	Glu	Ile	Tyr	Ile	Gln
1				5				10					15		
Ala	Lys	Asp	Lys	Gly	Ala	Asn	Pro	Glu	Gly	Ala	His	Cys	Lys	Val	Leu
	20					25						30			
Val	Glu	Val	Val	Asp	Val	Asn	Asp	Asn	Ala	Pro					
		35				40									

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGGGTTTGG ACTTTGAGCA AGTAGATGTC TACAAAATCC GCGTTGACGC GACGGACAAA	60
GGACACCCCTC CGATGGCAGG CCATTGCACT GTTTTAGTGA GGGTATTGGA TGAAAACGAC	120
AATGCGCCTC T	131

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Gly Leu Asp Phe Glu Gln Val Asp Val Tyr Lys Ile Arg Val Asp
1 5 10 15

Ala Thr Asp Lys Gly His Pro Pro Met Ala Gly His Cys Thr Val Leu
20 25 30

Val Arg Val Leu Asp Glu Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAGGGTATAG ACTTCGAGCA GATCAAGGAC TTCAGCTTTC AAGTGGAAAGC CCGGGACGCC 60
GGCAGTCCCC AGGCCTGTTC CGGCAACTGC ACTGTCAACA TCTTGATAGT GGATCAGAAC 120
GACAACGCC CTAA 134

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Lys Gly Ile Asp Phe Glu Gln Ile Lys Asp Phe Ser Phe Gln Val Glu
1 5 10 15

Ala Arg Asp Ala Gly Ser Pro Gln Ala Leu Ala Gly Asn Thr Thr Val
20 25 30

Asn Ile Leu Ile Val Asp Gln Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAGCCGTTCG ACTATGAGCA AACCGCCAAC ACGCTGGCAC AGATTGACGC CGTGCTGGAA 60
AAACAGGGCA GCAATAAAC GAGCATTCTG GATGCCACCA TTTTCCCTGGC CGATAAAAAC 120
GACAATGCGC CAGA 134

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys Pro Phe Asp Tyr Glu Gln Thr Ala Asn Thr Leu Ala Gln Ile Asp
1 5 10 15
Ala Val Leu Glu Lys Gln Gly Ser Asn Lys Ser Ser Ile Leu Asp Ala
20 25 30
Thr Ile Phe Leu Ala Asp Lys Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAGCGGCTGG ATTCGAACA GTTCCAGCAG CACAAAGCTGC TCGTAAGGGC TGTTGATGGA	60
GGAATGCCGC CACTGAGCAG CGATGTGGTC GTCACTGTGG ATGTCACCGA CCTCAACGAT	120
AACGCGCCCT A	131

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Lys Arg Leu Asp Phe Glu Gln Phe Gln Gln His Lys Leu Leu Val Arg	
1 5 10 15	
Ala Val Asp Gly Gly Met Pro Pro Leu Ser Ser Asp Val Val Val Thr	
20 25 30	
Val Asp Val Thr Asp Leu Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGGGGATAG ACTTGAGAG TGAGAATTAC TATGAATTG ATGTGCGGGC TCGCGATGGG	60
GGTTCTCCAG CCATGGAGCA ACATTGCAGC CTTCGAGTGG ATCTGCTGGA CGTAAATGAC	120
AACGCCAAC T	131

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Gly Ile Asp Phe Glu Ser Glu Asn Tyr Tyr Glu Phe Asp Val Arg
1 5 10 15

Ala Arg Asp Gly Gly Ser Pro Ala Met Glu Gln His Cys Ser Leu Arg
20 25 30

Val Asp Leu Leu Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAGGCATTGG ACTTTGAGGC CCGCGACTG TATTCGCTGA CAGTTCAAGGC CACGGACCGA 60
GGCGTGCCCT CGCTCACCGG GCGTGCCGAA GCGCTTATCC AGCTGCTAGA TGTCAACGAC 120
AACGCACCCA T 131

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Lys Ala Leu Asp Phe Glu Ala Arg Arg Leu Tyr Ser Leu Thr Val Gln
1 5 10 15

Ala Thr Asp Arg Gly Val Pro Ser Leu Thr Gly Arg Ala Glu Ala Leu
20 25 30

Ile Gln Leu Leu Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AAGCCAATTG ATTACGAGGC AACTCCATAC TATAACATGG AAATTGTAGC CACAGACAGC	60
GGAGGTCTT CGGGAAAATG CACTGTGTCT ATACAGGTGG TGGATGTGAA CGACAACGCC	120
CCCAA	125

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Lys Pro Ile Asp Tyr Glu Ala Thr Pro Tyr Tyr Asn Met Glu Ile Val	
1 5 10 15	

Ala Thr Asp Ser Gly Gly Leu Ser Gly Lys Cys Thr Val Ser Ile Gln	
20 25 30	

Val Val Asp Val Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGCGGGTAG ACTTCGAAAT GTGCAAAAGA TTTTACCTTG TGGTGGAAAGC TAAAGACGGA	60
GGCACCCCCAG CCCTCAGCAC GGCAAGCCACT GTCAGCATCG ACCTCACAGA TGTGAATGAT	120

AACCCCTCCTC	GGTTCAAGCCA	AGATGTCTAC	AGTGCTGTCA	TCAGTGAGGA	TGCCTTAGAG	180
GGGGACTCTG	TCATTCTGCT	GATAGCAGAA	GATGTGGATA	GCAAGCCTAA	TGGACAGATT	240
CGGTTTCCA	TCGTGGGTGG	AGATAGGGAC	AATGAATTG	CTGTCGATCC	AATCTTGGGA	300
CTTGTGAAAG	TTAAGAAGAA	ACTGGACCGG	GAGCGGGTGT	CAGGATACTC	CCTGCTCATC	360
CAGGCAGTAG	ATAGTGGCAT	TCCTGCAATG	TCCTCAACGA	CAACTGTCAA	CATTGATATT	420
TCTGATGTGA	ACGACAACGC	CCCCCT				446

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Lys Arg Val Asp Phe Glu Met Cys Lys Arg Phe Tyr Leu Val Val Glu
1 5 10 15

Ala Lys Asp Gly Gly Thr Pro Ala Leu Ser Thr Ala Ala Thr Val Ser
20 25 30

Ile Asp Leu Thr Asp Val Asn Asp Asn Pro Pro Arg Phe Ser Gln Asp
35 40 45

Val Tyr Asp Ala Val Ile Ser Glu Asp Ala Leu Glu Gly Asp Ser Val
50 55 60

Ile Leu Leu Ile Ala Glu Asp Val Asp Ser Lys Pro Asn Gly Gln Ile
65 70 75 80

Arg Phe Ser Ile Val Gly Gly Asp Arg Asp Asn Glu Phe Ala Val Asp
85 90 95

Pro Ile Leu Gly Leu Val Lys Val Lys Lys Lys Leu Asp Arg Glu Arg
100 105 110

Val Ser Gly Tyr Ser Leu Leu Ile Gln Ala Val Asp Ser Gly Ile Pro
115 120 125

Ala Met Ser Ser Thr Thr Val Asn Ile Asp Ile Ser Asp Val Asn
130 135 140

Asp Asn Ala Pro
145

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGGGGGTTG ATTATGAGAC AAACCCACGG CTACGACTGG TGCTACAGGC AGAGAGTGG	60
GGAGGCCCTTG CTTTCTCGGT GCTGACCCCTG ACCCTTCAG ATGCCAATGA CAATGCTCCC	120
CGTTTCCTGC AGCCTCACTA CGTGGCTTTG CTGCCAGAGT CCCGACCCTT GGAAGGGCCC	180
CTGCTGCAGG TGGAAAGCAGA CGACCTGGAT CAAGGCTCTG GAGGACAGAT CTCCTACAGT	240
CTGGCTGCAT CCCAGCCAGC ACGGGGCTTG TTCCATGTAG ACCCAGCCAC AGGCACATATC	300
ACTACCACAG CCATCCTGGA CCGGGAAATC TGGGCTGAAA CACGGCTGGT ACTGATGGCC	360
ACAGACAGAG GAAGCCCAGC ATTGGTGGGC TCAGCTACCC TGACAGTGAT GGTCACTCGAT	420
ACCAAACGACA ATGCTCCCC	440

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Lys	Gly	Val	Asp	Tyr	Glu	Thr	Asn	Pro	Arg	Leu	Arg	Leu	Val	Leu	Gln
1				5					10					15	
Ala	Glu	Ser	Gly	Gly	Ala	Phe	Ala	Phe	Ser	Val	Leu	Thr	Leu	Thr	Leu
	20					25						30			
Gln	Asp	Ala	Asn	Asp	Asn	Ala	Pro	Arg	Phe	Leu	Gln	Pro	His	Tyr	Val
		35					40					45			
Ala	Phe	Leu	Pro	Glu	Ser	Arg	Pro	Leu	Glu	Gly	Pro	Leu	Leu	Gln	Val
		50				55					60				
Glu	Ala	Asn	Asp	Leu	Asp	Gln	Gly	Ser	Gly	Gly	Gln	Ile	Ser	Tyr	Ser
	65				70				75				80		
Leu	Ala	Ala	Ser	Gln	Pro	Ala	Arg	Gly	Leu	Phe	His	Val	Asp	Pro	Ala
					85				90				95		

Thr Gly Thr Ile Thr Thr Ala Ile Leu Asp Arg Glu Ile Trp Ala
100 105 110

Glu Thr Arg Leu Val Leu Met Ala Thr Asp Arg Gly Ser Pro Ala Leu
115 120 125

Val Gly Ser Ala Thr Leu Thr Val Met Val Ile Asp Thr Asn Asp Asn
130 135 140

Ala Pro
145

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAGGTCTCGA TTATGAGGCA ACTCCATATT ATAACGTGGA AATTGTAGCC ACAGATGGTG 60

GGGGCCTTTC AGGAAAATGC ACTGTGGCTA TAGAAGTGGT GGATGTGAAC GACGGCGCTC 120

CAAT 124

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Gly Leu Asp Tyr Glu Ala Thr Pro Tyr Tyr Asn Val Glu Ile Val
1 5 10 15

Ala Thr Asp Gly Gly Ala Phe Asp Glu Asn Cys Thr Val Ala Ile Glu
20 25 30

Val Val Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Asp Xaa Asn Glu Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Asp Xaa Asp Glu Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Asp Xaa Asn Asp Asn Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AAGCGGATGG ATTTGAAGA CACCAAAC	T CATGAGATT ACATCCAGGC CAAAGACAAA	60
GGTGCCAATC CCGAAGGAGC GCATTGCAA	GTACTTGTAG AGGTTGTAGA CGTAAACGAC	120
AACGCCAG T		131

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Leu Arg Met Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr Ile Gln			
1	5	10	15
Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys Val Leu			
20	25	30	
Val Glu Val Val Asp Val Asn Asp Asn Ala Pro			
35	40		

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAGGCTTG ATTACGAGGA TCAGAGAGAG TTCCAACCAA CAGCTCATAT AAACGACGGA	60
GGTACCCAG TCTTAGCCAC CAACATCAGC GTGAACGTAT TTGTTACTGA CCGCAATGAT	120
AACGCCCT A	131

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys Ala Leu Asp Tyr Glu Asp Gln Arg Glu Phe Gln Leu Thr Ala His
1 5 10 15

Ile Asn Asp Gly Gly Thr Pro Val Leu Ala Thr Asn Ile Ser Val Asn
20 25 30

Val Phe Val Thr Asp Arg Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAGCGCTTGG ACTACGAGGA GAGTAACAAT TATGAAATTAC ACGTGGATGC TACAGATAAA 60
GGATACCCAC CTATGGTTGC TCACTGCACC GTACTCGTGG GAATCTTGGG TGAAAATGAC 120
AACGCACCCA T 131

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Lys Arg Leu Asp Tyr Glu Glu Ser Asn Asn Tyr Glu Ile His Val Asp
1 5 10 15

Ala Thr Asp Lys Gly Tyr Pro Pro Met Val Ala His Cys Thr Val Leu
20 25 30

Val Gly Ile Leu Asp Glu Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAACCGGTGG ACTACGAGAA AGTCAAAGAC TATACCATCG AGATCGTGGC TGTGGATTCC	60
GGCAACCCCTC CACTCTCTAG CACCAAACCTCC CTCAAGGTGC AGGTGGTAGA CGTCAACGAT	120
AACGCCCTC T	131

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Lys Pro Val Asp Tyr Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val	
1 5 10 15	
Ala Val Asp Ser Gly Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys	
20 25 30	
Val Gln Val Val Asp Val Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AAGCCTTTG ATTCGAGGA CACCAAACTC CATGAGATTT ACATCCAGGC CAAAGACAAG	60
GGCGCCAATC CGAAGGAGC ACATTGCAA GTGTTGGTGG AGGTTGTGGA TGTGAACGAC	120

AATGCCCTC A

131

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Lys Pro Phe Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr Ile Gln
1 5 10 15

Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys Val Leu
20 25 30

Val Glu Val Val Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

AAAGGTGTCG ATTACGAGGT GAGTCCACGG CTGCGACTGG TGCTGCAGGC AGAGAGTCGA 60
GGAGCCTTG CCTTCACTGT GCTGACCCTG ACCCTGCAAG ATGCCAACGA CAACGCCCG 120
AG 122

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Lys Gly Val Asp Tyr Glu Val Ser Pro Arg Leu Arg Leu Val Leu Gln
1 5 10 15

Ala Glu Ser Arg Gly Ala Phe Ala Phe Thr Val Leu Thr Leu Thr Leu
20 25 30

Gln Asp Ala Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AAAGGGATTG ATTACGAGCA GTTGAGAGAC CTACAGCTGT GGGTGACAGC CAGCGACAGC 60
GGGGACCCGC CTCTTAGCAG CAACGTGTCA CTGAGCCTGT TTGTGCTGGA CCAGAACGAC 120
AACGCCCCCC T 131

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Lys Gly Ile Asp Tyr Glu Gln Leu Arg Asp Leu Gln Leu Trp Val Thr
1 5 10 15

Ala Ser Asp Ser Gly Asp Pro Pro Leu Ser Ser Asn Val Ser Leu Ser
20 25 30

Leu Phe Val Leu Asp Gln Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAGGCGGTCTG ATTTTGAGCG CACATCCTCT TATCAACTCA TCATTCAGGC CACCAATATG	60
GCAGGAATGG CTTCCAATGC TACAGTCAAT ATTCAAGATTG TTGATGAAAA CGACAACGCC	120
CCCCA	125

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Lys Ala Val Asp Phe Glu Arg Thr Ser Ser Tyr Gln Leu Ile Ile Gln	
1 5 10 15	
Ala Thr Asn Met Ala Gly Met Ala Ser Asn Ala Thr Val Asn Ile Gln	
20 25 30	
Ile Val Asp Glu Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AAACGGCTAG ACTTTGAAAA GATACAAAAA TATGTTGTAT GGATAGAGGC CAGAGATGGT	60
GGTTTCCCTC CTTTCTCCTC TTACGAGAAA CTTGATATAA CAGTATTAGA TGTCAACGAT	120
AACGCGCCTA A	131

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Lys Arg Leu Asp Phe Glu Lys Ile Gln Lys Tyr Val Val Trp Ile Glu
1 5 10 15

Ala Arg Asp Gly Gly Phe Pro Pro Phe Ser Ser Tyr Glu Lys Leu Asp
20 25 30

Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AAGGGGATCG ATTATGAGAA GGTCAAAGAC TACACCATTG AGATTGTGGC TGTGGACTCT 60
GGCAACCCCC CACTCTCCAG CACTAACTCC CTCAAGGTGC AGGTGGTGGA CGTCAATGAC 120
AACGCACCGT G 131

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Lys Gly Ile Asp Tyr Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val
1 5 10 15

Ala Val Asp Ser Gly Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys
20 25 30

Val Gln Val Val Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

AAGGGACTCG ACTACGAGGA TCGGCAGGAA TTTGAATTAA CAGCTCATAT CAGCGATGGG	60
GGCACCCCGG TCCTAGCCAC CAACATCAGC GTGAACATAT TTGTCAGTGA TCGCAACGAT	120
AATGCCCGG T	131

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys	Gly	Leu	Asp	Tyr	Glu	Asp	Arg	Arg	Glu	Phe	Glu	Leu	Thr	Ala	His
1				5				10					15		
Ile	Ser	Asp	Gly	Gly	Thr	Pro	Val	Leu	Ala	Thr	Asn	Ile	Ser	Val	Asn
		20					25					30			
Ile	Phe	Val	Thr	Asp	Arg	Asn	Asp	Asn	Ala	Pro					
		35				40									

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AAGGGTTTGG ACTACGAGAC CACACAGGCC TACCAAGCTCA CGGTCAACGC CACAGATCAA	60
GACAACACCA GGCCTCTGTC CACCCTGGCC AACTTGGCCA TCATCATCAC AGATGTCCAG	120

GACATGGACC CCATCTTCAT CAACCTGCCT TACAGCACCA ACATCTACGA GCATTCTCCT	180
CGGGGCACGA CGGTGCGCAT CATCACCGCC ATAGACCAGG ATCAAGGACG TCCCCGGGGC	240
ATTGGCTACA CCATCGTTTC AGGGAATACC AACAGCATCT TTGCCCTGGA CTACATCAGC	300
GGAGTGCTGA CCTTGAATGG CCTGCTGGAC CGGGAGAACCC CCGTGTACAG CCATGGCTTC	360
ATCCTGACTG TGAAGGGCAC GGAGCTGAAC GATGACCGCA CCCCATCTGA CGCTACAGTC	420
ACCACGACCT TCAATATCCT GGTTATTGAC ATCAACGACA ACGCCCCACT	470

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Gly Leu Asp Tyr Glu Thr Thr Gln Ala Tyr Gln Leu Thr Val Asn			
1	5	10	15
Ala Thr Asp Gln Asp Asn Thr Arg Pro Leu Ser Thr Leu Ala Asn Leu			
20	25	30	
Ala Ile Ile Ile Thr Asp Val Gln Asp Met Asp Pro Ile Phe Ile Asn			
35	40	45	
Leu Pro Tyr Ser Thr Asn Ile Tyr Glu His Ser Pro Pro Gly Thr Thr			
50	55	60	
Val Arg Ile Ile Thr Ala Ile Asp Gln Asp Gln Gly Arg Pro Arg Gly			
65	70	75	80
Ile Gly Tyr Thr Ile Val Ser Gly Asn Thr Asn Ser Ile Phe Ala Leu			
85	90	95	
Asp Tyr Ile Ser Gly Val Leu Thr Leu Asn Gly Leu Leu Asp Arg Glu			
100	105	110	
Asn Pro Leu Tyr Ser Gly Gly Phe Ile Leu Thr Val Lys Gly Thr Glu			
115	120	125	
Leu Asn Asp Asp Arg Thr Pro Ser Asp Ala Thr Val Thr Thr Thr Phe			
130	135	140	
Asn Ile Leu Val Ile Asp Ile Asn Asp Asn Ala Pro			
145	150	155	

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AAGGGGGTCG ATTACGAGGT ACTACAGGCC TTTGAGTTCC ACGTGAGCGC CACAGACCAG	60
GGCTCACCGG GGCTCAGCAG CCAGGCTCTG GTGCGCGTGG TGGTGCTGGA CGACAATGAC	120
AACGCTCCCG T	131

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Lys Gly Val Asp Tyr Glu Val Leu Gln Ala Phe Glu Phe His Val Ser	
1 5 10 15	
Ala Thr Asp Arg Gly Ser Pro Gly Leu Ser Ser Gln Ala Leu Val Arg	
20 25 30	
Val Val Val Leu Asp Asp Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AAGGGGCTGG ATTATGAGCA GTTCCAGACC CTACAACTGG GAGTGACCGC TAGTGACAGT	60
GGAAACCCAC CATTAAGAAG CAATATTCA CTGACCCCTT TCGTGCTGGA CCAGAACATGAT	120

AACGCCCAA A

131

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Lys Gly Leu Asp Tyr Glu Gln Phe Gln Thr Leu Gln Leu Gly Val Thr
1 5 10 15
Ala Ser Asp Ser Gly Asn Pro Pro Leu Arg Ser Asn Ile Ser Leu Thr
20 25 30
Leu Phe Val Leu Asp Gln Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AAGCGGGTTG ATTACGAGGA TGTCCAGAAA TACTCGCTGA GCATTAAGGC CCAGGATGGG 60
CGGCCCGCGC TCATCAATTTC TTCAAGGGTG GTGTCTGTGC AGGTGCTGGA TGTCAACGAC 120
AATGCCCGG A 131

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Lys Arg Val Asp Tyr Glu Asp Val Gln Lys Tyr Ser Leu Ser Ile Lys
1 5 10 15

Ala	Gln	Asp	Gly	Arg	Pro	Pro	Leu	Ile	Asn	Ser	Ser	Gly	Val	Val	Ser
20								25					30		
Val	Gln	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala	Pro					
35							40								

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AAACCCGGTAG	ACTTTGAGCT	ACAGCAGTTC	TATGAAGTAG	CTGTGGTGGC	TTGGAACCTCT	60
GAGGGATTTC	ATGTCAAAAG	GGTCATTAAA	GTGCAACTTT	TAGATGACAA	CGACAATGCC	120
CCGAT						125

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys	Pro	Val	Asp	Phe	Glu	Leu	Gln	Gln	Phe	Tyr	Glu	Val	Ala	Val	Val
1				5					10			15			
Ala	Trp	Asn	Ser	Glu	Gly	Phe	His	Val	Lys	Arg	Val	Ile	Lys	Val	Gln
		20					25					30			
Leu	Leu	Asp	Asp	Asn	Asp	Asn	Ala	Pro							
		35				40									

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGGGATTAG ATTTTGAAC TTTGCCATT TACACATTGA TAATACAAGG AACTAACATG	60
GCTGGTTGT CCACTAATAC AACGGTTCTA GTTCACTTGC AGGATGAGAA TGATAACGCC	120
CCAAA	125

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Lys Gly Leu Asp Phe Glu Thr Leu Pro Ile Tyr Thr Leu Ile Ile Gln			
1	5	10	15
Gly Thr Asn Met Ala Gly Leu Ser Thr Asn Thr Thr Val Leu Val His			
20	25	30	
Leu Gln Asp Glu Asn Asp Asn Ala Pro			
35	40		

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AAGCGGGCGG ATTCGAGGC GATCGGGAG TACAGTCTGA GGATCAAAGC GCAGGACGGG	60
GGCGGGCCTC CCCTCAGCAA CACCACGGGC ATGGTCACAG TGCAGGTCGT GGACGTCAAT	120
GACAACGCAC CCCT	134

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Lys Arg Ala Asp Phe Glu Ala Ile Arg Glu Tyr Ser Leu Arg Ile Lys
1 5 10 15

Ala Gln Asp Gly Gly Arg Pro Pro Leu Ser Asn Thr Thr Gly Met Val
20 25 30

Thr Val Gln Val Val Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AAGCGGTTGG ATTACGAAAA GGCATCGGAA TATGAAATCT ATGTTCAAGC CGCTGACAAA 60
GGCGCTGTCC CTATGGCTGG CCATTGCAAA GTGTTGCTGG AGATCGTGG A TGTCAACGAC 120
AACGCCCT T 131

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Lys Arg Leu Asp Tyr Glu Lys Ala Ser Glu Tyr Glu Ile Tyr Val Gln
1 5 10 15

Ala Ala Asp Lys Gly Ala Val Pro Met Ala Gly His Cys Lys Val Leu
20 25 30

Leu Glu Ile Val Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AAGGGGATCG ATTATGAGGA TCAGGTCTCT TACACATTAG CAGTAACAGC ACATGACTAT	60
GGCATCCCTC AAAAATCAGA CACTACCTAT TTGGAAATCT TAGTAATTGA TGTTAACGAC	120
AACGCGCCCC A	131

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Lys Gly Ile Asp Tyr Glu Asp Gln Val Ser Tyr Thr Leu Ala Val Thr	
1 5 10 15	
Ala His Asp Tyr Gly Ile Pro Gln Lys Ser Asp Thr Thr Tyr Leu Glu	
20 25 30	
Ile Leu Val Ile Asp Val Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

AAAGGGTTAG ATTCGAGGG CACTAAAGAT TCAGCGTTA AAATAGTGGC AGCTGACACA	60
GGGAAGCCCA GCCTCAACCA GACAGCCCTG GTGAGAGTAG AGCTGGAGGA TGAGAACGAC	120

AACGCCCAA T

131

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys Gly Leu Asp Phe Glu Gly Thr Lys Asp Ser Ala Phe Lys Ile Val
1 5 10 15

Ala Ala Asp Thr Gly Lys Pro Ser Leu Asn Gln Thr Ala Leu Val Arg
20 25 30

Val Glu Leu Glu Asp Glu Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AAGGGTGTGG ATTTTGAAAG TGTGCGTAGC TACAGGCTGG TTATTCGTGC TCAAGATGGA 60

GGCAGCCCT CCAGAAGTAA CACCACCCAG CTCTTGGTCA ACGTCATCGA TCGAATGACA 120

ATGCGCCGCT 130

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Lys Gly Val Asp Phe Glu Ser Val Arg Ser Tyr Arg Leu Val Ile Arg
1 5 10 15

Ala Gln Asp Gly Gly Ser Pro Ser Arg Ser Asn Thr Thr Gln Leu Leu
20 25 30

Val Asn Val Ile Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AAGGGTGTGG ACTTCGAGCT GACACATCTG TATGAGATT GGATTGAGGC TGCCGATGGA 60
GACACGCCAA GTCTGCGTAG TGTAACTCTT ATAACGCTCA ACGTAACGGA TGCCAATGAC 120
AATGCTCCCA A 131

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Lys Gly Val Asp Phe Glu Leu Thr His Leu Tyr Glu Ile Trp Ile Glu
1 5 10 15
Ala Ala Asp Gly Asp Thr Pro Ser Leu Arg Ser Val Thr Leu Ile Thr
20 25 30
Leu Asn Val Thr Asp Ala Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAAGGCCTT GATTTGAAG AGACAAGTAG ATATGTGTTG AGTGTGGAAG CTAAGGATGG	60
AGGAGTACAC ACAGCTCACT GTAATGTTCA AATAGAAATT GTTGACGAGA ATGACAATGC	120
CCAGAGGTG ACATTCTCATGT CCTTCTCTAA CCAGATTCCA GAGGATTCAAG ACCTTGAAAC	180
TGTAATAGCC CTCATAAAAG TGCGAGACAA GGATTCTGGG CAAAATGGCA TGGTGACATG	240
CTATACTCAG GAAGAAGITC CTTCAAATT AGAATCCACC TCGAAGAATT ATTACAAGCT	300
GGTGATTGCT GGAGCCCTAA ACCGGGAGCA GACAGCAGAC TACAACGTCA CAATCATAGC	360
CACCGACAAG GGCAAACCAAG CCCTTTCTC CAGGACAAGC ATCACCCCTGC ACATCTCCGA	420
CATCAACGAT AATGCCCG T	441

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Lys Ala Phe Asp Phe Glu Glu Thr Ser Arg Tyr Val Leu Ser Val Glu			
1	5	10	15
Ala Lys Asp Gly Gly Val His Thr Ala His Cys Asn Val Gln Ile Glu			
20	25	30	
Ile Val Asp Glu Asn Asp Asn Ala Pro Glu Val Thr Phe Met Ser Phe			
35	40	45	
Ser Asn Gln Ile Pro Glu Asp Ser Asp Leu Gly Thr Val Ile Ala Leu			
50	55	60	
Ile Lys Val Arg Asp Lys Asp Ser Gly Gln Asn Gly Met Val Thr Cys			
65	70	75	80
Tyr Thr Gln Glu Glu Val Pro Phe Lys Leu Glu Ser Thr Ser Lys Asn			
85	90	95	
Tyr Tyr Lys Leu Val Ile Ala Gly Ala Leu Asn Arg Glu Gln Thr Ala			
100	105	110	
Asp Tyr Asn Val Thr Ile Ile Ala Thr Asp Lys Gly Lys Pro Ala Leu			
115	120	125	
Ser Ser Arg Thr Ser Ile Thr Leu His Ile Ser Asp Ile Asn Asp Asn			
130	135	140	
Ala Pro			
145			

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

AAGCGAGTGG ATTACGAGGC CACTCGGAAT TATAAGCTGA GAGTTAAGGC TACTGATCTT	60
GGGATTCCAC CGAGATCTTC TAACATGACA CTGTTCATTC ATGTCCCTGA TGTAAACGAC	120
AACGCTCCCT T	131

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Lys Arg Val Asp Tyr Glu Ala Thr Arg Asn Tyr Lys Leu Arg Val Lys	
1 5 10 15	
Ala Thr Asp Leu Gly Ile Pro Pro Arg Ser Ser Asn Met Thr Leu Phe	
20 25 30	
Ile His Val Leu Asp Val Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 495..3572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTCTATTCTG ACATTCTCTT TGGATTGTT TGCTATAACT TGAAATTTGG GATGTCACAA	60
ACGAAACTGT CATCTGTTTC CGCCAAACTG TGGTTCTGCT AATCTCCCAG GCTGGCAGCA	120
TTGGAGACTT GCTGACTTCT TTCATCCCCC ACTCTTTCA CCTGAAATTG CTTTCCTTGG	180
TTTGCTCTA AGTCCTATGC TTCAGTCAGG GGCCAACCAA ATCTCACTGC CTCCTTTTA	240
TCATGAAGCC TTTGATCACT GATAGTTCTT TTTATATCTT GAAAAATCAC CCTTCCCAGT	300
ACAGTTAATA TTTAGTATCT CTACTCATCT TGGCACTTAC TCACAGCTCC ATAATTCACT	360
CGTTTCGTA CCTCTTCATG GTGATGGGA GCCCTTTGGA GGTGGTGACT GTGCTTTATA	420
CTCCTCATGA TGCTTCACAT GTGGCAGGCC TGGAGTGCCTT GGAGGCGGCC CTCCTGATT	480
TGGGCCCTCC CAGG ATG GAG CCC CTG AGG CAC AGC CCA GGC CCT GGG GGG	530
Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly	
1 5 10	
CAA CGG CTA CTG CTG CCC TCC ATG CTG CTA GCA CTG CTG CTC CTG CTG	578
Gln Arg Leu Leu Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu Leu	
15 20 25	
GCT CCA TCC CCA GGC CAC GCC ACT CGG GTA GTG TAC AAG GTG CCG GAG	626
Ala Pro Ser Pro Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu	
30 35 40	
GAA CAG CCA CCC AAC ACC CTC ATT GGG AGC CTC GCA GCC GAC TAT GGT	674
Glu Gln Pro Pro Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly	
45 50 55 60	
TTT CCA GAT GTG GGG CAC CTG TAC AAG CTA GAG GTG GGT GCC CCG TAC	722
Phe Pro Asp Val Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr	
65 70 75	
CTT CGC GTG GAT GGC AAG ACA GGT GAC ATT TTC ACC ACC GAG ACC TCC	770
Leu Arg Val Asp Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser	
80 85 90	
ATC GAC CGT GAG GGG CTC CGT GAA TGC CAG AAC CAG CTC CCT GGT GAT	818
Ile Asp Arg Glu Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp	
95 100 105	
CCC TGC ATC CTG GAG TTT GAG GTA TCT ATC ACA GAC CTC GTG CAG AAT	866
Pro Cys Ile Leu Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn	
110 115 120	
GCG AGC CCC CGG CTG CTA GAG GGC CAG ATA GAA GTA CAA GAC ATC AAT	914
Ala Ser Pro Arg Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn	
125 130 135 140	
GAC AAC ACA CCC AAC TTC GCC TCA CCA GTC ATC ACT CTG GCC ATC CCT	962
Asp Asn Thr Pro Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro	
145 150 155	
GAG AAC ACC AAC ATC GGC TCA CTC TTC CCC ATC CCG CTG GCT TCA GAC	1010
Glu Asn Thr Asn Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp	
160 165 170	

CGT GAT GCT GGT CCC AAC GGT GTG GCA TCC TAT GAG CTG CAG GTG GCA Arg Asp Ala Gly Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala	1058
175 180 185	
GAG GAC CAG GAG GAG AAG CAA CCA CAG CTC ATT GTG ATG GGC AAC CTG Glu Asp Gln Glu Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu	1106
190 195 200	
GAC CGT GAG CGC TGG GAC TCC TAT GAC CTC ACC ATC AAG GTG CAG GAT Asp Arg Glu Arg Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp	1154
205 210 215 220	
GGC GGC AGC CCC CCA CGC GCC ACG AGT GCC CTG CTG CGT GTC ACC GTG Gly Gly Ser Pro Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val	1202
225 230 235	
CTT GAC ACC AAT GAC AAC GCC CCC AAG TTT GAG CGG CCC TCC TAT GAG Leu Asp Thr Asn Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu	1250
240 245 250	
GCC GAA CTA TCT GAG AAT AGC CCC ATA GGC CAC TCG GTC ATC CAG GTG Ala Glu Leu Ser Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val	1298
255 260 265	
AAG GCC AAT GAC TCA GAC CAA GGT GCC AAT GCA GAA ATC GAA TAC ACA Lys Ala Asn Asp Ser Asp Gln Gly Ala Asn Ala Glu Ile Glu Tyr Thr	1346
270 275 280	
TTC CAC CAG GCG CCC GAA GTT GTG AGG CGT CTT CTT CGA CTG GAC AGG Phe His Gln Ala Pro Glu Val Val Arg Arg Leu Leu Arg Leu Asp Arg	1394
285 290 295 300	
AAC ACT GGA CTT ATC ACT GTT CAG GGC CCG GTG GAC CGT GAG GAC CTA Asn Thr Gly Leu Ile Thr Val Gln Gly Pro Val Asp Arg Glu Asp Leu	1442
305 310 315	
AGC ACC CTG CGC TTC TCA GTG CTT GCT AAG GAC CGA GGC ACC AAC CCC Ser Thr Leu Arg Phe Ser Val Leu Ala Lys Asp Arg Gly Thr Asn Pro	1490
320 325 330	
AAG AGT GCC CGT GCC CAG GTG GTT GTG ACC GTG AAG GAC ATG AAT GAC Lys Ser Ala Arg Ala Gln Val Val Val Thr Val Lys Asp Met Asn Asp	1538
335 340 345	
AAT GCC CCC ACC ATT GAG ATC CGG GGC ATA GGG CTA GTG ACT CAT CAA Asn Ala Pro Thr Ile Glu Ile Arg Gly Ile Gly Leu Val Thr His Gln	1586
350 355 360	
GAT GGG ATG GCT AAC ATC TCA GAG GAT GTG GCA GAG GAG ACA GCT GTG Asp Gly Met Ala Asn Ile Ser Glu Asp Val Ala Glu Glu Thr Ala Val	1634
365 370 375 380	
GCC CTG GTG CAG GTG TCT GAC CGA GAT GAG GGA GAG AAT GCA GCT GTC Ala Leu Val Gln Val Ser Asp Arg Asp Glu Gly Glu Asn Ala Ala Val	1682
385 390 395	
ACC TGT GTG GTG GCA GGT GAT GTG CCC TTC CAG CTG CGC CAG GCC AGT Thr Cys Val Val Ala Gly Asp Val Pro Phe Gln Leu Arg Gln Ala Ser	1730
400 405 410	

GAG ACA GGC AGT GAC AGC AAG AAG AAG TAT TTC CTG CAG ACT ACC ACC Glu Thr Gly Ser Asp Ser Lys Lys Lys Tyr Phe Leu Gln Thr Thr Thr 415 420 425	1778
CCG CTA GAC TAC GAG AAG GTC AAA GAC TAC ACC ATT GAG ATT GTG GCT Pro Leu Asp Tyr Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val Ala 430 435 440	1826
GTG GAC TCT GGC AAC CCC CCA CTC TCC AGC ACT AAC TCC CTC AAG GTG Val Asp Ser Gly Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys Val 445 450 455 460	1874
CAG GTG GTG GAC GTC AAT GAC AAC GCA CCT GTC TTC ACT CAG AGT GTC Gln Val Val Asp Val Asn Asp Asn Ala Pro Val Phe Thr Gln Ser Val 465 470 475	1922
ACT GAG GTC GCC TTC CCG GAA AAC AAC AAG CCT GGT GAA GTG ATT GCT Thr Glu Val Ala Phe Pro Glu Asn Asn Lys Pro Gly Glu Val Ile Ala 480 485 490	1970
GAG ATC ACT GCC AGT GAT GCT GAC TCT GGC TCT AAT GCT GAG CTG GTT Glu Ile Thr Ala Ser Asp Ala Asp Ser Gly Ser Asn Ala Glu Leu Val 495 500 505	2018
TAC TCT CTG GAG CCT GAG CCG GCT GCT AAG GGC CTC TTC ACC ATC TCA Tyr Ser Leu Glu Pro Glu Pro Ala Ala Lys Gly Leu Phe Thr Ile Ser 510 515 520	2066
CCC GAG ACT GGA GAG ATC CAG GTG AAG ACA TCT CTG GAT CGG GAA CAG Pro Glu Thr Gly Glu Ile Gln Val Lys Thr Ser Leu Asp Arg Glu Gln 525 530 535 540	2114
CGG GAG AGC TAT GAG TTG AAG GTG GTG GCA GCT GAC CGG GGC AGT CCT Arg Glu Ser Tyr Glu Leu Lys Val Val Ala Ala Asp Arg Gly Ser Pro 545 550 555	2162
AGC CTC CAG GGC ACA GCC ACT GTC CTT GTC AAT GTG CTG GAC TGC AAT Ser Leu Gln Gly Thr Ala Thr Val Leu Val Asn Val Leu Asp Cys Asn 560 565 570	2210
GAC AAT GAC CCC AAA TTT ATG CTG AGT GGC TAC AAC TTC TCA GTG ATG Asp Asn Asp Pro Lys Phe Met Leu Ser Gly Tyr Asn Phe Ser Val Met 575 580 585	2258
GAG AAC ATG CCA GCA CTG AGT CCA GTG GGC ATG GTG ACT GTC ATT GAT Glu Asn Met Pro Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp 590 595 600	2306
GGA GAC AAG GGG GAG AAT GCC CAG GTG CAG CTC TCA GTG GAG CAG GAC Gly Asp Lys Gly Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp 605 610 615 620	2354
AAC GGT GAC TTT GTT ATC CAG AAT GGC ACA GGC ACC ATC CTA TCC AGC Asn Gly Asp Phe Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser 625 630 635	2402
CTG AGC TTT GAT CGA GAG CAA CAA AGC ACC TAC ACC TTC CAG CTG AAG Leu Ser Phe Asp Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys 640 645 650	2450

GCA GTG GAT GGT GGC GTC CCA CCT CGC TCA GCT TAC GTT GGT GTC ACC Ala Val Asp Gly Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr 655 660 665	2498
ATC AAT GTG CTG GAC GAG AAT GAC AAC GCA CCC TAT ATC ACT GCC CCT Ile Asn Val Leu Asp Glu Asn Asp Asn Ala Pro Tyr Ile Thr Ala Pro 670 675 680	2546
TCT AAC ACC TCT CAC AAG CTG CTG ACC CCC CAG ACA CGT CTT GGT GAG Ser Asn Thr Ser His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu 685 690 695 700	2594
ACG GTC AGC CAG GTG GCA GCC GAG GAC TTT GAC TCT GGT GTC AAT GCC Thr Val Ser Gln Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala 705 710 715	2642
GAG CTG ATC TAC AGC ATT GCA GGT GGC AAC CCT TAT GGA CTC TTC CAG Glu Leu Ile Tyr Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln 720 725 730	2690
ATT GGG TCA CAT TCA GGT GCC ATC ACC CTG GAG AAG GAG ATT GAG CGG Ile Gly Ser His Ser Gly Ala Ile Thr Leu Glu Lys Glu Ile Glu Arg 735 740 745	2738
CGC CAC CAT GGG CTA CAC CGC CTG GTG GTG AAG GTC AGT GAC CGC GGC Arg His His Gly Leu His Arg Leu Val Val Lys Val Ser Asp Arg Gly 750 755 760	2786
AAG CCC CCA CGC TAT GGC ACA GCC TTG GTC CAT CTT TAT GTC AAT GAG Lys Pro Pro Arg Tyr Gly Thr Ala Leu Val His Leu Tyr Val Asn Glu 765 770 775 780	2834
ACT CTG GCC AAC CGC ACG CTG CTG GAG ACC CTC CTG GGC CAC AGC CTG Thr Leu Ala Asn Arg Thr Leu Leu Glu Thr Leu Leu Gly His Ser Leu 785 790 795	2882
GAC ACG CCG CTG GAT ATT GAC ATT GCT GGG GAT CCA GAA TAT GAG CGC Asp Thr Pro Leu Asp Ile Asp Ile Ala Gly Asp Pro Glu Tyr Glu Arg 800 805 810	2930
TCC AAG CAG CGT GGC AAC ATT CTC TTT GGT GTG GTG GCT GGT GTG GTG Ser Lys Gln Arg Gly Asn Ile Leu Phe Gly Val Val Ala Gly Val Val 815 820 825	2978
GCC GTG GCC TTG CTC ATC GCC CTG GCG GTT CTT GTG CGC TAC TGC AGA Ala Val Ala Leu Leu Ile Ala Leu Ala Val Leu Val Arg Tyr Cys Arg 830 835 840	3026
CAG CGG GAG GCC AAA AGT GGT TAC CAG GCT GGT AAG AAG GAG ACC AAG Gln Arg Glu Ala Lys Ser Gly Tyr Gln Ala Gly Lys Lys Glu Thr Lys 845 850 855 860	3074
GAC CTG TAT GCC CCC AAG CCC AGT GGC AAG GCC TCC AAG GGA AAC AAA Asp Leu Tyr Ala Pro Lys Pro Ser Gly Lys Ala Ser Lys Gly Asn Lys 865 870 875	3122
AGC AAA GGC AAG AAG AGC AAG TCC CCA AAG CCC GTG AAG CCA GTG GAG Ser Lys Gly Lys Lys Ser Lys Ser Pro Lys Pro Val Lys Pro Val Glu 880 885 890	3170

GAC GAG GAT GAG GCC GGG CTG CAG AAG TCC CTC AAG TTC AAC CTG ATG Asp Glu Asp Glu Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met 895 900 905	3218
AGC GAT GCC CCT GGG GAC AGT CCC CGC ATC CAC CTG CCC CTC AAC TAC Ser Asp Ala Pro Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr 910 915 920	3266
CCA CCA GGC AGC CCT GAC CTG GGC CGC CAC TAT CGC TCT AAC TCC CCA Pro Pro Gly Ser Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro 925 930 935 940	3314
CTG CCT TCC ATC CAG CTG CAG CCC CAG TCA CCC TCA GCC TCC AAG AAG Leu Pro Ser Ile Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys 945 950 955	3362
CAC CAG GTG GTA CAG GAC CTG CCA CCT GCA AAC ACA TTC GTG GGC ACC His Gln Val Val Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr 960 965 970	3410
GGG GAC ACC ACG TCC ACG GGC TCT GAG CAG TAC TCC GAC TAC AGC TAC Gly Asp Thr Thr Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr 975 980 985	3458
CGC ACC AAC CCC CCC AAA TAC CCC AGC AAG CAG GTA GGC CAG CCC TTT Arg Thr Asn Pro Pro Lys Tyr Pro Ser Lys Gln Val Gly Gln Pro Phe 990 995 1000	3506
CAG CTC AGC ACA CCC CAG CCC CTA CCC CAC CCC TAC CAC GGA GCC ATC Gln Leu Ser Thr Pro Gln Pro Leu Pro His Pro Tyr His Gly Ala Ile 1005 1010 1015 1020	3554
TGG ACC GAG GTG TGG GAG TGATGGAGCA GGTTTACTGT GCCTGCCCGT Trp Thr Glu Val Trp Glu 1025	3602
GTTGGGGGCC AGCCTGAGCC AGCAGTGGGA GGTGGGGCCT TAGTGCCTCA CCGGGCACAC	3662
GGATTAGGCT GAGTGAAGAT TAAGGGAGGG TGTGCTCTGT GGTCTCCTCC CTGCCCTCTC	3722
CCC ACTGGGG AGAGACCTGT GATTTGCCAA GTCCCTGGAC CCTGGACCAG CTACTGGCC	3782
TTATGGGTTG GGGGTGGTAG GCAGGTGAGC GTAAGTGGGG AGGGAAATGG GTAAGAAGTC	3842
TACTCCAAAC CTAGGTCTCT ATGTCAGACC AGACCTAGGT GCTTCTCTAG GAGGGAAACA	3902
GGGAGACCTG GGGCTCTGTG GATAACTGAG TGGGGAGTCT GCCAGGGAG GGCACCTTCC	3962
CATTGTGCCT TCTGTGTGA TTGTGCATTA ACCTCTTCCT CACCACTAGG CTTCTGGGC	4022
TGGGTCCCCAC ATGCCCTTGA CCCTGACAAT AAAGTTCTCT ATTGAA AAAAAAAA AAAAAAA AAAAAAAA AA	4082
	4104

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly Gln Arg Leu Leu
1 5 10 15

Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu Ala Pro Ser Pro
20 25 30

Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu Glu Gln Pro Pro
35 40 45

Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly Phe Pro Asp Val
50 55 60

Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr Leu Arg Val Asp
65 70 75 80

Gly Lys Thr Gly Asp Ile Phe Thr Glu Thr Ser Ile Asp Arg Glu
85 90 95

Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp Pro Cys Ile Leu
100 105 110

Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn Ala Ser Pro Arg
115 120 125

Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn Asp Asn Thr Pro
130 135 140

Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro Glu Asn Thr Asn
145 150 155 160

Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp Arg Asp Ala Gly
165 170 175

Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala Glu Asp Gln Glu
180 185 190

Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu Asp Arg Glu Arg
195 200 205

Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp Gly Gly Ser Pro
210 215 220

Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val Leu Asp Thr Asn
225 230 235 240

Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu Ala Glu Leu Ser
245 250 255

Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val Lys Ala Asn Asp
260 265 270

Ser Asp Gln Gly Ala Asn Ala Glu Ile Glu Tyr Thr Phe His Gln Ala
275 280 285

Pro Glu Val Val Arg Arg Leu Leu Arg Leu Asp Arg Asn Thr Gly Leu
290 295 300

Ile Thr Val Gln Gly Pro Val Asp Arg Glu Asp Leu Ser Thr Leu Arg
305 310 315 320

Phe Ser Val Leu Ala Lys Asp Arg Gly Thr Asn Pro Lys Ser Ala Arg
325 330 335

Ala Gln Val Val Val Thr Val Lys Asp Met Asn Asp Asn Ala Pro Thr
340 345 350

Ile Glu Ile Arg Gly Ile Gly Leu Val Thr His Gln Asp Gly Met Ala
355 360 365

Asn Ile Ser Glu Asp Val Ala Glu Glu Thr Ala Val Ala Leu Val Gln
370 375 380

Val Ser Asp Arg Asp Glu Gly Glu Asn Ala Ala Val Thr Cys Val Val
385 390 395 400

Ala Gly Asp Val Pro Phe Gln Leu Arg Gln Ala Ser Glu Thr Gly Ser
405 410 415

Asp Ser Lys Lys Tyr Phe Leu Gln Thr Thr Thr Pro Leu Asp Tyr
420 425 430

Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val Ala Val Asp Ser Gly
435 440 445

Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys Val Gln Val Val Asp
450 455 460

Val Asn Asp Asn Ala Pro Val Phe Thr Gln Ser Val Thr Glu Val Ala
465 470 475 480

Phe Pro Glu Asn Asn Lys Pro Gly Glu Val Ile Ala Glu Ile Thr Ala
485 490 495

Ser Asp Ala Asp Ser Gly Ser Asn Ala Glu Leu Val Tyr Ser Leu Glu
500 505 510

Pro Glu Pro Ala Ala Lys Gly Leu Phe Thr Ile Ser Pro Glu Thr Gly
515 520 525

Glu Ile Gln Val Lys Thr Ser Leu Asp Arg Glu Gln Arg Glu Ser Tyr
530 535 540

Glu Leu Lys Val Val Ala Ala Asp Arg Gly Ser Pro Ser Leu Gln Gly
545 550 555 560

Thr Ala Thr Val Leu Val Asn Val Leu Asp Cys Asn Asp Asn Asp Pro
565 570 575

Lys Phe Met Leu Ser Gly Tyr Asn Phe Ser Val Met Glu Asn Met Pro
580 585 590

Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp Gly Asp Lys Gly
595 600 605

Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp Asn Gly Asp Phe
610 615 620

Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser Leu Ser Phe Asp
625 630 635 640

Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys Ala Val Asp Gly
645 650 655

Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr Ile Asn Val Leu
660 665 670

Asp Glu Asn Asp Asn Ala Pro Tyr Ile Thr Ala Pro Ser Asn Thr Ser
675 680 685

His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu Thr Val Ser Gln
690 695 700

Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala Glu Leu Ile Tyr
705 710 715 720

Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln Ile Gly Ser His
725 730 735

Ser Gly Ala Ile Thr Leu Glu Lys Glu Ile Glu Arg Arg His His Gly
740 745 750

Leu His Arg Leu Val Val Lys Val Ser Asp Arg Gly Lys Pro Pro Arg
755 760 765

Tyr Gly Thr Ala Leu Val His Leu Tyr Val Asn Glu Thr Leu Ala Asn
770 775 780

Arg Thr Leu Leu Glu Thr Leu Leu Gly His Ser Leu Asp Thr Pro Leu
785 790 795 800

Asp Ile Asp Ile Ala Gly Asp Pro Glu Tyr Glu Arg Ser Lys Gln Arg
805 810 815

Gly Asn Ile Leu Phe Gly Val Val Ala Gly Val Val Ala Val Ala Leu
820 825 830

Leu Ile Ala Leu Ala Val Leu Val Arg Tyr Cys Arg Gln Arg Glu Ala
835 840 845

Lys Ser Gly Tyr Gln Ala Gly Lys Lys Glu Thr Lys Asp Leu Tyr Ala
850 855 860

Pro Lys Pro Ser Gly Lys Ala Ser Lys Gly Asn Lys Ser Lys Gly Lys
865 870 875 880

Lys Ser Lys Ser Pro Lys Pro Val Lys Pro Val Glu Asp Glu Asp Glu
885 890 895

Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met Ser Asp Ala Pro
900 905 910

Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr Pro Pro Gly Ser
915 920 925

Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro Leu Pro Ser Ile
930 935 940

Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys His Gln Val Val
945 950 955 960

Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr Gly Asp Thr Thr
965 970 975

Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr Arg Thr Asn Pro
980 985 990

Pro Lys Tyr Pro Ser Lys Gln Val Gly Gln Pro Phe Gln Leu Ser Thr
995 1000 1005

Pro Gln Pro Leu Pro His Pro Tyr His Gly Ala Ile Trp Thr Glu Val
1010 1015 1020

Trp Glu
1025

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 115..2827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CGAAAGCCAT GTCGGACTCG TCGCCCAGCG CCCAACGCT AACCCGCTGA AAGTTTCTCA 60

GCGAAATCTC AGGGACGATC TGGACCCCGC TGAGAGGAAC TGCTTTGAG TGAG ATG 117
Met
1

GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG 165
Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val
5 10 15

GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT 213
Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile
20 25 30

CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC 261
His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn
35 40 45

GTG GTC GCG AAC CTT GGT TTG GAT CTC GGT AGC CTC TCA GCC CGC AGG Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg Arg 50 55 60 65	309
TTC CCG GTG GTG TCT GGA GCT AGC CGA AGA TTC TTT GAG GTG AAC CGG Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn Arg 70 75 80	357
GAG ACC GGA GAG ATG TTT GTG AAC GAC CGT CTG GAT CGA GAG GAG CTG Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu Leu 85 90 95	405
TGT GGG ACA CTG CCC TCT TGC ACT GTA ACT CTG GAG TTG GTA GTG GAG Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val Glu 100 105 110	453
AAC CCG CTG GAG CTG TTC AGC GTG GAA GTG GTG ATC CAG GAC ATC AAC Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile Asn 115 120 125	501
GAC AAC AAT CCT GCT TTC CCT ACC CAG GAA ATG AAA TTG GAG ATT AGC Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile Ser 130 135 140 145	549
GAG GCC GTG GCT CCG GGG ACG CGC TTT CCG CTC GAG AGC GCG CAC GAT Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His Asp 150 155 160	597
CCC GAT CTG GGA AGC AAC TCT TTA CAA ACC TAT GAG CTG AGC CGA AAT Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg Asn 165 170 175	645
GAA TAC TTT GCG CTT CGC GTG CAG ACG CGG GAG GAC AGC ACC AAG TAC Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys Tyr 180 185 190	693
GCG GAG CTG GTG TTG GAG CGC GCC CTG GAC CGA GAA CGG GAG CCT AGT Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro Ser 195 200 205	741
CTC CAG TTA GTG CTG ACG GCG TTG GAC GGA GGG ACC CCA GCT CTC TCC Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu Ser 210 215 220 225	789
GCC AGC CTG CCT ATT CAC ATC AAG GTG CTG GAC GCG AAT GAC AAT GCG Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn Ala 230 235 240	837
CCT GTC TTC AAC CAG TCC TTG TAC CGG GCG CGC GTT CCT GGA GGA TGC Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly Cys 245 250 255	885
ACC TCC GGC ACG CGC GTG GTA CAA GTC CTT GCA ACG GAT CTG GAT GAA Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp Glu 260 265 270	933
GGC CCC AAC GGT GAA ATT ATT TAC TCC TTC GGC AGC CAC AAC CGC GCC Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg Ala 275 280 285	981

GGC GTG CGG CAA CTA TTC GCC TTA GAC CTT GTA ACC GGG ATG CTG ACA Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu Thr 290 295 300 305	1029
ATC AAG GGT CGG CTG GAC TTC GAG GAC ACC AAA CTC CAT GAG ATT TAC Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr 310 315 320	1077
ATC CAG GCC AAA GAC AAG GGC GCC AAT CCC GAA GGA GCA CAT TGC AAA Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys 325 330 335	1125
GTG TTG GTG GAG GTT GTG GAT GTG AAT GAC AAC GCC CCG GAG ATC ACA Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile Thr 340 345 350	1173
GTC ACC TCC GTG TAC AGC CCA GTA CCC GAG GAT GCC TCT GGG ACT GTC Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr Val 355 360 365	1221
ATC GCT TTG CTC AGT GTG ACT GAC CTG GAT GCT GGC GAG AAC GGG CTG Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly Leu 370 375 380 385	1269
GTG ACC TGC GAA GTT CCA CCG GGT CTC CCT TTC AGC CTT ACT TCT TCC Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser Ser 390 395 400	1317
CTC AAG AAT TAC TTC ACT TTG AAA ACC AGT GCA GAC CTG GAT CGG GAG Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg Glu 405 410 415	1365
ACT GTG CCA GAA TAC AAC CTC AGC ATC ACC GCC CGA GAC GCC GGA ACC Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly Thr 420 425 430	1413
CCT TCC CTC TCA GCC CTT ACA ATA GTG CGT GTT CAA GTG TCC GAC ATC Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp Ile 435 440 445	1461
AAT GAC AAC CCT CCA CAA TCT TCT CAA TCT TCC TAC GAC GTT TAC ATT Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr Ile 450 455 460 465	1509
GAA GAA AAC AAC CTC CCC GGG GCT CCA ATA CTA AAC CTA AGT GTC TGG Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val Trp 470 475 480	1557
GAC CCC GAC GCC CCG CAG AAT GCT CGG CTT TCT TTC TTT CTC TTG GAG Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu Glu 485 490 495	1605
CAA GGA GCT GAA ACC GGG CTA GTG GGT CGC TAT TTC ACA ATA AAT CGT Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn Arg 500 505 510	1653
GAC AAT GGC ATA GTG TCA TCC TTA GTG CCC CTA GAC TAT GAG GAT CGG Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp Arg 515 520 525	1701

CGG GAA TTT GAA TTA ACA GCT CAT ATC AGC GAT GGG GGC ACC CCG GTC Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro Val 530 535 540 545	1749
CTA GCC ACC AAC ATC AGC GTG AAC ATA TTT GTC ACT GAT CGC AAT GAC Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn Asp 550 555 560	1797
AAT GCC CCC CAG GTC CTA TAT CCT CGG CCA GGT GGG AGC TCG GTG GAG Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val Glu 565 570 575	1845
ATG CTG CCT CGA GGT ACC TCA GCT GGC CAC CTA GTG TCA CGG GTG GTA Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val Val 580 585 590	1893
GGC TGG GAC GCG GAT GCA GGG CAC AAT GCC TGG CTC TCC TAC AGT CTC Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser Leu 595 600 605	1941
TTT GGA TCC CCT AAC CAG AGC CTT TTT GCC ATA GGG CTG CAC ACT GGT Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr Gly 610 615 620 625	1989
CAA ATC AGT ACT GCC CGT CCA GTC CAA GAC ACA GAT TCA CCC AGG CAG Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg Gln 630 635 640	2037
ACT CTC ACT GTC TTG ATC AAA GAC AAT GGG GAG CCT TCG CTC TCC ACC Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser Thr 645 650 655	2085
ACT GCT ACC CTC ACT GTG TCA GTA ACC GAG GAC TCT CCT GAA GCC CGA Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala Arg 660 665 670	2133
GCC GAG TTC CCC TCT GGC TCT GCC CCC CGG GAG CAG AAA AAA AAT CTC Ala Glu Phe Pro Ser Gly Ser Ala Pro Arg Glu Gln Lys Lys Asn Leu 675 680 685	2181
ACC TTT TAT CTA CTT CTT TCT CTA ATC CTG GTT TCT GTG GGC TTC GTG Thr Phe Tyr Leu Leu Ser Leu Ile Leu Val Ser Val Gly Phe Val 690 695 700 705	2229
GTC ACA GTG TTC GGA GTA ATC ATA TTC AAA GTT TAC AAG TGG AAG CAG Val Thr Val Phe Gly Val Ile Ile Phe Lys Val Tyr Lys Trp Lys Gln 710 715 720	2277
TCT AGA GAC CTA TAC CGA GCC CCG GTG AGC TCA CTG TAC CGA ACA CCA Ser Arg Asp Leu Tyr Arg Ala Pro Val Ser Ser Leu Tyr Arg Thr Pro 725 730 735	2325
GGG CCC TCC TTG CAC GCG GAC GCC GTG CGG GGA GGC CTG ATG TCG CCG Gly Pro Ser Leu His Ala Asp Ala Val Arg Gly Gly Leu Met Ser Pro 740 745 750	2373
CAC CTT TAC CAT CAG GTG TAT CTC ACC ACG GAC TCC CGC CGC AGC GAC His Leu Tyr His Gln Val Tyr Leu Thr Thr Asp Ser Arg Arg Ser Asp 755 760 765	2421

CCG CTG CTG AAG AAA CCT GGT GCA GCC AGT CCA CTG GCC AGC CGC CAG Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg Gln 770 775 780 785	2469
AAC ACG CTG CGG AGC TGT GAT CCG GTG TTC TAT AGG CAG GTG TTG GGT Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu Gly 790 795 800	2517
GCA GAG AGC GCC CCT CCC GGA CAG CAA GCC CCG CCC AAC ACG GAC TGG Ala Glu Ser Ala Pro Pro Gly Gln Gln Ala Pro Pro Asn Thr Asp Trp 805 810 815	2565
CGT TTC TCT CAG GCC CAG AGA CCC GGC ACC AGC GGC TCC CAA AAT GGC Arg Phe Ser Gln Ala Gln Arg Pro Gly Thr Ser Gly Ser Gln Asn Gly 820 825 830	2613
GAT GAC ACC GGC ACC TGG CCC AAC AAC CAG TTT GAC ACA GAG ATG CTG Asp Asp Thr Gly Thr Trp Pro Asn Asn Gln Phe Asp Thr Glu Met Leu 835 840 845	2661
CAA GCC ATG ATC TTG GCG TCC GCC AGT GAA GCT GCT GAT GGG AGC TCC Gln Ala Met Ile Leu Ala Ser Ala Ser Glu Ala Ala Asp Gly Ser Ser 850 855 860 865	2709
ACC CTG GGA GGG GGT GCC GGC ACC ATG GGA TTG AGC GCC CGC TAC GGA Thr Leu Gly Gly Ala Gly Thr Met Gly Leu Ser Ala Arg Tyr Gly 870 875 880	2757
CCC CAG TTC ACC CTG CAG CAC GTG CCC GAC TAC CGC CAG AAT GTC TAC Pro Gln Phe Thr Leu Gln His Val Pro Asp Tyr Arg Gln Asn Val Tyr 885 890 895	2805
ATC CCA GGC AGC AAT GCA CAC T GACCAACGCA GCTGGCAAGC GGATGGCAAG Ile Pro Gly Ser Asn Ala His 900	2857
GCCCCAGCAGG TGGCAATGGC AACAAAGAAGA AGTCGGCAAG AAGGAGAAGA AGTAACATGG AGGCCAGGCC AAGAGCCACA GGGCAGCCTC TCCCCGAACC AGCCCAGCTT CTCCCTTACCT GCACCCAGGC CTCAGAGTTT CAGGGCTAAC CCCCAGAATA CTGGTAGGGG CCAAGGCATC TCCCTTGAA ACAGAAACAA GTGCCATCAC ACCATCCCTT CCCCAGGTGT AATATCCAAA GCAGTTCCGC TGGGAACCCC ATCCAATCAG TGGCTGTACC CATTGGGTA GTGGGGTTCA TGTAGACACC AAGAACCAT TGCACACCCC CGTTAGTTA CAGCTGAACC CTCCATCTTC CAAATCAATC AGGCCCATCC ATCCCATGCC TCCCTCCTCC CCACCCCCACT CCAACAGTTC CTCTTCCCG AGTAAGGTGG TTGGGGTGTT GAAGTACCAA GTAACCTACA AGCCTCCTAG TTCTGAAAAG TTGGAAAGGGC ATCATGACCT CTTGGCCTCT CCTTTGATTC TCAATCTTCC CCCAAAGCAT GGTTGGTGC CAGCCCCCTTC ACCTCCTTCC AGAGCCCAAG ATCAATGCTC AAGTTTGGA GGACATGATC ACCATCCCCA TGGTACTGAT GCTTGCTGGA TTTAGGGAGG GCATTTGCT ACCAAGCCTC TTCCCAACGC CCTGGGACCA GTCTTCTGTT TTGTTTTCA TTGTTTGAGC TTTCCACTGC ATGCCCTTGAC TTCCCCCACC TCCTCCTCAA ACAAGAGACT	2917 2977 3037 3097 3157 3217 3277 3337 3397 3457 3517 3577 3637

CCACTGCATG TTCCAAGACA GTATGGGTG GTAAGATAAG GAAGGGAAGT GTGTGGATGT	3697
GGATGGTGGG GGCATGGACA AAGCTTGACA CATCAAGTTA TCAAGGCCCT GGAGGGAGGCT	3757
CTGTATGTCC TCAGGGACT GACAACATCC TCCAGATTCC AGCCATAAAC CAATAACTAG	3817
GCTGGACCCT TCCCCTACA TAATAGGGCT CAGCCAGGCA GCCAGCTTG GGCTGAGCTA	3877
ACAGGACCAA TGGATTAACG GGCATTTCAAG TCCAAGGAAG CTCGAAGCAG GTTTAGGACC	3937
AGGTCCCCCTT GAGAGGTCAG AGGGGCCTCT GTGGGTGCTG GGTACTCCAG AGGTGCCACT	3997
GGTGGAAAGGG TCAGCGGAGC CCCAGCAGGA AGGGTGGGCC AGCCAGGCCA TTCTTAGTCC	4057
CTGGGTTGGG GAGGCAGGGA GCTAGGGCAG GGACCAAATG AACAGAAAGT CTCAGCCCAG	4117
GATGGGGCTT CTTCAACAGG CCCCTGCCCT CCTGAAGCCT CAGTCCTTCA CCTTGCCAGG	4177
TGCCGTTCT CTTCCGTGAA GGCCACTGCC CAGGTCCCCA GTGCGCCCCC TAGTGGCCAT	4237
AGCCTGGTTA AAGTTCCCCA GTGCCCTCCTT GTGATAGACC TTCTTCTCCC ACCCCCTTCT	4297
GCCCCCTGGGT CCCCGGCCAT CCAGCGGGGC TGCCAGAGAA CCCCAGACCT GCCCTTACAG	4357
TAGTGTAGCG CCCCCCTCCCT CTTTCGGCTG GTGTAGAATA GCCAGTAGTG TAGTGCAGGTG	4417
TGCTTTTACG TGATGGGGGG TGGGCAGCGG GCAGCGCGT CCGCGCAGCC GTCTGTCCCT	4477
GATCTGCCCG CGGCAGGCCCG TGTTGTGTTT TGTGCTGTGT CCAGCGCTAA GGCGACCCCC	4537
TCCCCCGTAC TGACTTCTCC TATAAGCGCT TCTCTCGCA TAGTCACGTA GCTCCCACCC	4597
CACCCCTTTC CTGTGTCTCA CGCAAGTTT ATACTCTAAT ATTATATATGG CTTTTTTCT	4657
TCGACAAAAA AATAATAAAA CGTTTCTTCT GAAAAAAA AAAAAAAA	4705

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val	
1 5 10 15	
Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val	
20 25 30	
Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly	
35 40 45	
Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg	
50 55 60	

Arg Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn
65 70 75 80

Arg Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu
85 90 95

Leu Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val
100 105 110

Glu Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile
115 120 125

Asn Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile
130 135 140

Ser Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His
145 150 155 160

Asp Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg
165 170 175

Asn Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys
180 185 190

Tyr Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro
195 200 205

Ser Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu
210 215 220

Ser Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn
225 230 235 240

Ala Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly
245 250 255

Cys Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp
260 265 270

Glu Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg
275 280 285

Ala Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu
290 295 300

Thr Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile
305 310 315 320

Tyr Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys
325 330 335

Lys Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile
340 345 350

Thr Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr
355 360 365

Val Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly
370 375 380

Leu Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser
385 390 395 400

Ser Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg
405 410 415

Glu Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly
420 425 430

Thr Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp
435 440 445

Ile Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr
450 455 460

Ile Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val
465 470 475 480

Trp Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu
485 490 495

Glu Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn
500 505 510

Arg Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp
515 520 525

Arg Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro
530 535 540

Val Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn
545 550 555 560

Asp Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val
565 570 575

Glu Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val
580 585 590

Val Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser
595 600 605

Leu Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr
610 615 620

Gly Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg
625 630 635 640

Gln Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser
645 650 655

Thr Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala
660 665 670

Arg Ala Glu Phe Pro Ser Gly Ser Ala Pro Arg Glu Gln Lys Lys Asn
675 680 685

Leu Thr Phe Tyr Leu Leu Leu Ser Leu Ile Leu Val Ser Val Gly Phe
690 695 700

Val Val Thr Val Phe Gly Val Ile Ile Phe Lys Val Tyr Lys Trp Lys
705 710 715 720

Gln Ser Arg Asp Leu Tyr Arg Ala Pro Val Ser Ser Leu Tyr Arg Thr
725 730 735

Pro Gly Pro Ser Leu His Ala Asp Ala Val Arg Gly Gly Leu Met Ser
740 745 750

Pro His Leu Tyr His Gln Val Tyr Leu Thr Thr Asp Ser Arg Arg Ser
755 760 765

Asp Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg
770 775 780

Gln Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu
785 790 795 800

Gly Ala Glu Ser Ala Pro Pro Gly Gln Gln Ala Pro Pro Asn Thr Asp
805 810 815

Trp Arg Phe Ser Gln Ala Gln Arg Pro Gly Thr Ser Gly Ser Gln Asn
820 825 830

Gly Asp Asp Thr Gly Thr Trp Pro Asn Asn Gln Phe Asp Thr Glu Met
835 840 845

Leu Gln Ala Met Ile Leu Ala Ser Ala Ser Glu Ala Ala Asp Gly Ser
850 855 860

Ser Thr Leu Gly Gly Ala Gly Thr Met Gly Leu Ser Ala Arg Tyr
865 870 875 880

Gly Pro Gln Phe Thr Leu Gln His Val Pro Asp Tyr Arg Gln Asn Val
885 890 895

Tyr Ile Pro Gly Ser Asn Ala His
900

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Asp Trp Val Ile Pro Pro Ile Asn Leu Pro Glu Asn Ser Arg Gly Pro
1 5 10 15

Phe Pro Gln Glu Leu Val Arg Ile Arg Ser Asp Arg Asp Lys Asn Leu
20 25 30

Ser Leu Arg Tyr Thr Val Thr Gly Pro Gly Ala Asp Gln Pro Pro Thr
35 40 45

Gly Ile Phe Ile Ile Asn Pro Ile Ser Gly Gln Leu Ser Val Thr Lys
50 55 60

Pro Leu Asp Arg Glu Gln Ile Ala Arg Phe His Leu Arg Ala His Ala
65 70 75 80

Val Asp Ile Asn Gly Asn Gln Val Glu Asn Pro Ile Asp, Ile Val Ile
85 90 95

Asn Val Ile Asp Met Asn Asp Asn Arg Pro Glu Phe Leu His Gln Val
100 105 110

Trp Asn Gly Ser Val Pro Glu Gly Ser Lys Pro Gly Thr Tyr Val Met
115 120 125

Thr Val Thr Ala Ile Asp Ala Asp Asp Pro Asn Ala Leu Asn Gly Met
130 135 140

Leu Arg Tyr Arg Ile Leu Ser Gln Ala Pro Ser Thr Pro Ser Pro Asn
145 150 155 160

Met Phe Thr Ile Asn Asn Glu Thr Gly Asp Ile Ile Thr Val Ala Ala
165 170 175

Gly Leu Asp Arg Glu Lys Val Gln Gln Tyr Thr Leu Ile Ile Gln Ala
180 185 190

Thr Asp Met Glu Gly Asn Pro Thr Tyr Gly Leu Ser Asn Thr Ala Thr
195 200 205

Ala Val Ile Thr Val Thr Asp Val Asn Asp Asn Pro Pro Glu Phe Thr
210 215 220

Ala Met Thr Phe Tyr Gly Glu Val Pro Glu Asn Arg Val Asp Ile Ile
225 230 235 240

Val Ala Asn Leu Thr Val Thr Asp Lys Asp Gln Pro His Thr Pro Ala
245 250 255

Trp Asn Ala Val Thr Arg Ile Ser Gly Gly Asp Pro Thr Gly Arg Phe
260 265 270

Ala Ile Gln Thr Asp Pro Asn Ser Asn Asp Gly Leu Val Thr Val Val
275 280 285

Lys Pro Ile Asp Phe Glu Thr Asn Arg Met Phe Val Leu Thr Val Ala
290 295 300

Ala Glu Asn Gln Val Pro Leu Ala Lys Gly Ile Gln His Pro Pro Gln
305 310 315 320

Ser Thr Ala Thr Val Ser Val Thr Val Ile Asp Val Asn Glu Asn Pro
325 330 335

Tyr Phe Ala Pro Asn Pro Lys Ile Ile Arg Gln Glu Glu Gly Leu His
340 345 350

Ala Gly Thr Met Leu Thr Thr Phe Thr Ala Gly Asp Pro Asp Arg Tyr
355 360 365

Met Gln Gln Asn Ile Arg Tyr Thr Lys Leu Ser Asp Pro Ala Asn Trp
370 375 380

Leu Lys Ile Asp Pro Val Asn Gly Gln Ile Thr Thr Ile Ala Val Leu
385 390 395 400

Asp Arg Glu Ser Pro Asn Val Lys Asn Asn Ile Tyr Asn Ala Thr Phe
405 410 415

/ Leu Ala Ser Asp Asn Gly Ile Pro Pro Met Ser Gly Thr Gly Thr Leu
420 425 430

Gln Ile Tyr Leu Leu Asp Ile Asn Asp Asn Ala Pro Gln Val Leu Pro
435 440 445

Gln Glu Ala Glu Thr Cys Glu Thr Pro Asp Pro Asn Ser Ile Asn Ile
450 455 460

Thr Thr Ala Leu Asp Tyr Asp Ile Asp Pro Asn Ala Gly Pro Phe Ala
465 470 475 480

Tyr Asp Leu Pro Leu Ser Pro Val Thr Ile Lys Arg Asn Trp Thr Ile
485 490 495

Thr Arg Leu Asn Gly Asp Phe Ala Gln Leu Asn Leu Lys Ile Lys Phe
500 505 510

Leu Glu Ala Gly Ile Tyr Glu Val Pro Ile Ile Ile Thr Asp Ser Gly
515 520 525

Asn Pro Pro Lys Ser Asn Lys Ser Ile Leu Arg Val Arg Val Cys Gln
530 535 540

Cys Asp Phe Asn Gly Asp Cys Thr Asp Val Asp Arg
545 550 555

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Glu Asp Thr Val Tyr Ser Phe Asp Ile Pro Glu Asn Ala Gln Arg Gly
1 5 10 15

Tyr Gln Val Gly Gln Ile Val Ala Arg Asp Ala Asp Leu Gly Gln Asn
20 25 30

Ala Gln Leu Ser Tyr Gly Val Val Ser Asp Trp Ala Asn Asp Val Phe
35 40 45

Ser Leu Asn Pro Gln Thr Gly Met Leu Thr Leu Thr Ala Arg Leu Asp
50 55 60

Tyr Glu Glu Val Gln His Tyr Ile Leu Ile Val Gln Ala Gln Asp Asn
65 70 75 80

Gly Gln Pro Ser Leu Ser Thr Thr Ile Thr Val Tyr Cys Asn Val Leu
85 90 95

Asp Leu Asn Asp Asn Ala Pro Ile Phe
100 105

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Asp Xaa Asp Xaa Gly Xaa Asn
1 5

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ala Xaa Asp Xaa Gly Xaa Pro
1 5

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4650 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 495..4103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCTCTATTCTG ACATTCTCTT TGGATTGTT TGCTATAACT TGAAATTTGG GATGTCACAA	60
ACGAAACTGT CATCTGTTTC CGCCAAACTG TGGTTCTGCT AATCTCCCAG GCTGGCAGCA	120
TTGGAGACTT GCTGACTTCT TTCATCCCCC ACTCTTTCA CCTGAAATTG CTTTCCCTGG	180
TTTTGCTCTA AGTCCTATGC TTCAGTCAGG GGCCAACCAA ATCTCACTGC CTCCTTTTA	240
TCATGAAGCC TTTGATCACT GATAGTTCTT TTTATATCTT GAAAAATCAC CCTTCCCAGT	300
ACAGTTAATA TTTAGTATCT CTACTCATCT TGGCACTTAC TCACAGCTCC ATAATTCACT	360
CGTTTCGTA CCTCTTCATG GTGATGGGGA GCCCTTGGA GGTGGTGACT GTGCTTTATA	420
CTCCTCATGA TGCTTCACAT GTGGCAGGCG TGGAGTGCC GGAGGCGGCC CTCCTGATTC	480
TGGGCCCTCC CAGG ATG GAG CCC CTG AGG CAC AGC CCA GGC CCT GGG GGG Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly	530
1 5 10	
CAA CGG CTA CTG CTG CCC TCC ATG CTG CTA GCA CTG CTG CTC CTG CTG Gln Arg Leu Leu Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu Leu	578
15 20 25	
GCT CCA TCC CCA GGC CAC GCC ACT CGG GTA GTG TAC AAG GTG CCG GAG Ala Pro Ser Pro Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu	626
30 35 40	
GAA CAG CCA CCC AAC ACC CTC ATT GGG AGC CTC GCA GCC GAC TAT GGT Glu Gln Pro Pro Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly	674
45 50 55 60	
TTT CCA GAT GTG GGG CAC CTG TAC AAG CTA GAG GTG GGT GCC CCG TAC Phe Pro Asp Val Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr	722
65 70 75	
CTT CGC GTG GAT GGC AAG ACA GGT GAC ATT TTC ACC ACC GAG ACC TCC Leu Arg Val Asp Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser	770
80 85 90	
ATC GAC CGT GAG GGG CTC CGT GAA TGC CAG AAC CAG CTC CCT GGT GAT Ile Asp Arg Glu Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp	818
95 100 105	
CCC TGC ATC CTG GAG TTT GAG GTA TCT ATC ACA GAC CTC GTG CAG AAT Pro Cys Ile Leu Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn	866
110 115 120	
GCG AGC CCC CGG CTG CTA GAG GGC CAG ATA GAA GTA CAA GAC ATC AAT Ala Ser Pro Arg Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn	914
125 130 135 140	
GAC AAC ACA CCC AAC TTC GCC TCA CCA GTC ATC ACT CTG GCC ATC CCT Asp Asn Thr Pro Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro	962
145 150 155	
GAG AAC ACC AAC ATC GGC TCA CTC TTC CCC ATC CCG CTG GCT TCA GAC Glu Asn Thr Asn Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp	1010
160 165 170	

CGT GAT GCT GGT CCC AAC GGT GTG GCA TCC TAT GAG CTG CAG GTG GCA Arg Asp Ala Gly Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala	1058
175 180 185	
GAG GAC CAG GAG GAG AAG CAA CCA CAG CTC ATT GTG ATG GGC AAC CTG Glu Asp Gln Glu Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu	1106
190 195 200	
GAC CGT GAG CGC TGG GAC TCC TAT GAC CTC ACC ATC AAG GTG CAG GAT Asp Arg Glu Arg Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp	1154
205 210 215 220	
GGC GGC AGC CCC CCA CGC GCC ACG AGT GCC CTG CTG CGT GTC ACC GTG Gly Gly Ser Pro Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val	1202
225 230 235	
CTT GAC ACC AAT GAC AAC GCC CCC AAG TTT GAG CGG CCC TCC TAT GAG Leu Asp Thr Asn Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu	1250
240 245 250	
GCC GAA CTA TCT GAG AAT AGC CCC ATA GGC CAC TCG GTC ATC CAG GTG Ala Glu Leu Ser Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val	1298
255 260 265	
AAG GCC AAT GAC TCA GAC CAA GGT GCC AAT GCA GAA ATC GAA TAC ACA Lys Ala Asn Asp Ser Asp Gln Gly Ala Asn Ala Glu Ile Glu Tyr Thr	1346
270 275 280	
TTC CAC CAG GCG CCC GAA GTT GTG AGG CGT CTT CTT CGA CTG GAC AGG Phe His Gln Ala Pro Glu Val Val Arg Arg Leu Leu Arg Leu Asp Arg	1394
285 290 295 300	
AAC ACT GGA CTT ATC ACT GTT CAG GGC CCG GTG GAC CGT GAG GAC CTA Asn Thr Gly Leu Ile Thr Val Gln Gly Pro Val Asp Arg Glu Asp Leu	1442
305 310 315	
AGC ACC CTG CGC TTC TCA GTG CTT GCT AAG GAC CGA GGC ACC AAC CCC Ser Thr Leu Arg Phe Ser Val Leu Ala Lys Asp Arg Gly Thr Asn Pro	1490
320 325 330	
AAG AGT GCC CGT GCC CAG GTG GTT GTG ACC GTG AAG GAC ATG AAT GAC Lys Ser Ala Arg Ala Gln Val Val Val Thr Val Lys Asp Met Asn Asp	1538
335 340 345	
AAT GCC CCC ACC ATT GAG ATC CGG GGC ATA GGG CTA GTG ACT CAT CAA Asn Ala Pro Thr Ile Glu Ile Arg Gly Ile Gly Leu Val Thr His Gln	1586
350 355 360	
GAT GGG ATG GCT AAC ATC TCA GAG GAT GTG GCA GAG GAG ACA GCT GTG Asp Gly Met Ala Asn Ile Ser Glu Asp Val Ala Glu Glu Thr Ala Val	1634
365 370 375 380	
GCC CTG GTG CAG GTG TCT GAC CGA GAT GAG GGA GAG AAT GCA GCT GTC Ala Leu Val Gln Val Ser Asp Arg Asp Glu Gly Glu Asn Ala Ala Val	1682
385 390 395	
ACC TGT GTG GTG GCA GGT GAT GTG CCC TTC CAG CTG CGC CAG GCC AGT Thr Cys Val Val Ala Gly Asp Val Pro Phe Gln Leu Arg Gln Ala Ser	1730
400 405 410	

GAG ACA GGC AGT GAC AGC AAG AAG AAG TAT TTC CTG CAG ACT ACC ACC Glu Thr Gly Ser Asp Ser Lys Lys Lys Tyr Phe Leu Gln Thr Thr Thr 415 420 425	1778
CCG CTA GAC TAC GAG AAG GTC AAA GAC TAC ACC ATT GAG ATT GTG GCT Pro Leu Asp Tyr Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val Ala 430 435 440	1826
GTC GAC TCT GGC AAC CCC CCA CTC TCC AGC ACT AAC TCC CTC AAG GTG Val Asp Ser Gly Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys Val 445 450 455 460	1874
CAG GTG GTG GAC GTC AAT GAC AAC GCA CCT GTC TTC ACT CAG AGT GTC Gln Val Val Asp Val Asn Asp Asn Ala Pro Val Phe Thr Gln Ser Val 465 470 475	1922
ACT GAG GTC GCC TTC CCG GAA AAC AAC AAG CCT GGT GAA GTG ATT GCT Thr Glu Val Ala Phe Pro Glu Asn Asn Lys Pro Gly Glu Val Ile Ala 480 485 490	1970
GAG ATC ACT GCC AGT GAT GCT GAC TCT GGC TCT AAT GCT GAG CTG GTT Glu Ile Thr Ala Ser Asp Ala Asp Ser Gly Ser Asn Ala Glu Leu Val 495 500 505	2018
TAC TCT CTG GAG CCT GAG CCG GCT GCT AAG GGC CTC TTC ACC ATC TCA Tyr Ser Leu Glu Pro Glu Pro Ala Ala Lys Gly Leu Phe Thr Ile Ser 510 515 520	2066
CCC GAG ACT GGA GAG ATC CAG GTG AAG ACA TCT CTG GAT CGG GAA CAG Pro Glu Thr Gly Glu Ile Gln Val Lys Thr Ser Leu Asp Arg Glu Gln 525 530 535 540	2114
CGG GAG AGC TAT GAG TTG AAG GTG GTG GCA GCT GAC CGG GGC AGT CCT Arg Glu Ser Tyr Glu Leu Lys Val Val Ala Ala Asp Arg Gly Ser Pro 545 550 555	2162
AGC CTC CAG GGC ACA GCC ACT GTC CTT GTC AAT GTG CTG GAC TGC AAT Ser Leu Gln Gly Thr Ala Thr Val Leu Val Asn Val Leu Asp Cys Asn 560 565 570	2210
GAC AAT GAC CCC AAA TTT ATG CTG AGT GGC TAC AAC TTC TCA GTG ATG Asp Asn Asp Pro Lys Phe Met Leu Ser Gly Tyr Asn Phe Ser Val Met 575 580 585	2258
GAG AAC ATG CCA GCA CTG AGT CCA GTG GGC ATG GTG ACT GTC ATT GAT Glu Asn Met Pro Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp 590 595 600	2306
GGA GAC AAG GGG GAG AAT GCC CAG GTG CAG CTC TCA GTG GAG CAG GAC Gly Asp Lys Gly Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp 605 610 615 620	2354
AAC GGT GAC TTT GTT ATC CAG AAT GGC ACA GGC ACC ATC CTA TCC AGC Asn Gly Asp Phe Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser 625 630 635	2402
CTG AGC TTT GAT CGA GAG CAA CAA AGC ACC TAC ACC TTC CAG CTG AAG Leu Ser Phe Asp Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys 640 645 650	2450

GCA GTG GAT GGT GGC GTC CCA CCT CGC TCA GCT TAC GTT GGT GTC ACC Ala Val Asp Gly Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr 655 660 665	2498
ATC AAT GTG CTG GAC GAG AAT GAC AAC GCA CCC TAT ATC ACT GCC CCT Ile Asn Val Leu Asp Glu Asn Asp Asn Ala Pro Tyr Ile Thr Ala Pro 670 675 680	2546
TCT AAC ACC TCT CAC AAG CTG CTG ACC CCC CAG ACA CGT CTT GGT GAG Ser Asn Thr Ser His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu 685 690 695 700	2594
ACG GTC AGC CAG GTG GCA GCC GAG GAC TTT GAC TCT GGT GTC AAT GCC Thr Val Ser Gln Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala 705 710 715	2642
GAG CTG ATC TAC AGC ATT GCA GGT GGC AAC CCT TAT GGA CTC TTC CAG Glu Leu Ile Tyr Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln 720 725 730	2690
ATT GGG TCA CAT TCA GGT GCC ATC ACC CTG GAG AAG GAG ATT GAG CGG Ile Gly Ser His Ser Gly Ala Ile Thr Leu Glu Lys Glu Ile Glu Arg 735 740 745	2738
CGC CAC CAT GGG CTA CAC CGC CTG GTG GTG AAG GTC AGT GAC CGC GGC Arg His His Gly Leu His Arg Leu Val Val Lys Val Ser Asp Arg Gly 750 755 760	2786
AAG CCC CCA CGC TAT GGC ACA GCC TTG GTC CAT CTT TAT GTC AAT GAG Lys Pro Pro Arg Tyr Gly Thr Ala Leu Val His Leu Tyr Val Asn Glu 765 770 775 780	2834
ACT CTG GCC AAC CGC ACG CTG CTG GAG ACC CTC CTG GGC CAC AGC CTG Thr Leu Ala Asn Arg Thr Leu Leu Glu Thr Leu Leu Gly His Ser Leu 785 790 795	2882
GAC ACG CCG CTG GAT ATT GAC ATT GCT GGG GAT CCA GAA TAT GAG CGC Asp Thr Pro Leu Asp Ile Asp Ile Ala Gly Asp Pro Glu Tyr Glu Arg 800 805 810	2930
TCC AAG CAG CGT GGC AAC ATT CTC TTT GGT GTG GTG GCT GGT GTG GTG Ser Lys Gln Arg Gly Asn Ile Leu Phe Gly Val Val Ala Gly Val Val 815 820 825	2978
GCC GTG GCC TTG CTC ATC GCC CTG GCG GTT CTT GTG CGC TAC TGC AGA Ala Val Ala Leu Leu Ile Ala Leu Ala Val Leu Val Arg Tyr Cys Arg 830 835 840	3026
CAG CGG GAG GCC AAA AGT GGT TAC CAG GCT GGT AAG AAG GAG ACC AAG Gln Arg Glu Ala Lys Ser Gly Tyr Gln Ala Gly Lys Lys Glu Thr Lys 845 850 855 860	3074
GAC CTG TAT GCC CCC AAG CCC AGT GGC AAG GCC TCC AAG GGA AAC AAA Asp Leu Tyr Ala Pro Lys Pro Ser Gly Lys Ala Ser Lys Gly Asn Lys 865 870 875	3122
AGC AAA GGC AAG AAG AGC AAG TCC CCA AAG CCC GTG AAG CCA GTG GAG Ser Lys Gly Lys Ser Lys Ser Pro Lys Pro Val Lys Pro Val Glu 880 885 890	3170

GAC GAG GAT GAG GCC GGG CTG CAG AAG TCC CTC AAG TTC AAC CTG ATG Asp Glu Asp Glu Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met 895 900 905	3218
AGC GAT GCC CCT GGG GAC AGT CCC CGC ATC CAC CTG CCC CTC AAC TAC Ser Asp Ala Pro Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr 910 915 920	3266
CCA CCA GGC AGC CCT GAC CTG GGC CGC CAC TAT CGC TCT AAC TCC CCA Pro Pro Gly Ser Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro 925 930 935 940	3314
CTG CCT TCC ATC CAG CTG CAG CCC CAG TCA CCC TCA GCC TCC AAG AAG Leu Pro Ser Ile Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys 945 950 955	3362
CAC CAG GTG GTA CAG GAC CTG CCA CCT GCA AAC ACA TTC GTG GGC ACC His Gln Val Val Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr 960 965 970	3410
GGG GAC ACC ACG TCC ACG GGC TCT GAG CAG TAC TCC GAC TAC AGC TAC Gly Asp Thr Thr Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr 975 980 985	3458
CGC ACC AAC CCC CCC AAA TAC CCC AGC AAG CAG TTA CCT CAC CGC CGC Arg Thr Asn Pro Pro Lys Tyr Pro Ser Lys Gln Leu Pro His Arg Arg 990 995 1000	3506
GTC ACC TTC TCG GCC ACC AGC CAG GCC CAG GAG CTG CAG GAC CCA TCC Val Thr Phe Ser Ala Thr Ser Gln Ala Gln Glu Leu Gln Asp Pro Ser 1005 1010 1015 1020	3554
CAG CAC AGT TAC TAT GAC AGT GGC CTG GAG GAG TCT GAG ACG CCG TCC Gln His Ser Tyr Tyr Asp Ser Gly Leu Glu Glu Ser Glu Thr Pro Ser 1025 1030 1035	3602
AGC AAG TCA TCC TCA GGG CCT CGA CTC GGT CCC CTG GCC CTG CCT GAG Ser Lys Ser Ser Ser Gly Pro Arg Leu Gly Pro Leu Ala Leu Pro Glu 1040 1045 1050	3650
GAT CAC TAT GAG CGC ACC ACC CCT GAT GGC AGC ATA GGA GAG ATG GAG Asp His Tyr Glu Arg Thr Thr Pro Asp Gly Ser Ile Gly Glu Met Glu 1055 1060 1065	3698
CAC CCC GAG AAT GAC CTT CGC CCT TTG CCT GAT GTC GCC ATG ACA GGC His Pro Glu Asn Asp Leu Arg Pro Leu Pro Asp Val Ala Met Thr Gly 1070 1075 1080	3746
ACA TGT ACC CGG GAG TGC AGT GAG TTT GGC CAC TCT GAC ACA TGC TGG Thr Cys Thr Arg Glu Cys Ser Glu Phe Gly His Ser Asp Thr Cys Trp 1085 1090 1095 1100	3794
ATG CCT GGC CAG TCA TCT CCC AGC CGC CGG ACC AAG AGC AGC GCC CTC Met Pro Gly Gln Ser Ser Pro Ser Arg Arg Thr Lys Ser Ser Ala Leu 1105 1110 1115	3842
AAA CTC TCC ACC TTC ATG CCT TAC CAG GAC CGA GGA GGG CAG GAG CCT Lys Leu Ser Thr Phe Met Pro Tyr Gln Asp Arg Gly Gly Gln Glu Pro 1120 1125 1130	3890
GCG GGC GCC GGC AGC CCC AGC CCC CCG GAA GAC CGG AAC ACC AAA ACG Ala Gly Ala Gly Ser Pro Ser Pro Pro Glu Asp Arg Asn Thr Lys Thr	3938

1135	1140	1145	
GCC CCC GTG CGC CTC CTG CCC TCC TAC AGT GCC TTC TCC CAC AGT AGC Ala Pro Val Arg Leu Leu Pro Ser Tyr Ser Ala Phe Ser His Ser Ser 1150 1155 1160			3986
CAT GAT TCC TGC AAG GAC TCG GCC ACC TTG GAG GAA ATC CCC CTG ACC His Asp Ser Cys Lys Asp Ser Ala Thr Leu Glu Glu Ile Pro Leu Thr 1165 1170 1175 1180			4034
CAG ACC TCG GAC TTC CCA CCC GCA GCC ACA CCG GCA TCT GCC CAG ACG Gln Thr Ser Asp Phe Pro Pro Ala Ala Thr Pro Ala Ser Ala Gln Thr 1185 1190 1195			4082
GCC AAG CGC GAG ATC TAC CTG TGAGCCCCCT ACTGGCCGGC CCCCCCTCCCC Ala Lys Arg Glu Ile Tyr Leu 1200			4133
CAGCGCCGGC CAGCTCCCAA ATGCCCATTC CAGGGCCTCA CTCTCCACCC CTTCAGCGTG GAECTCCTGC CAGGGCCCAA GTGGGGGTAT CACTGACCTC ATGACCACGC TGGCCCTTCT CCCATGCAGG GTCCAGGTCC TCTCCCTCA TTTCCATCTC CCAGCCCAGG GGCCCTTCC CCTTTATGGG GCTTCCCCCA GCTGATGCCA AAGAGGGCTC CTCTGCAATG ACTGGGCTCC TTCCCTTGAC TTCCAGGGAG CACCCCTCG ATTTGGCAG ATGGTGGAGT CAAGGGTGGG CAGCGTACTT CTAACTCATT GTTCCCTCA TGGCCGACCA GGGCGGGGAT AGCATGCCA ATTTTAGCCC TGAAGCAGGG CTGAACCTGGG GAGCCCTTT CCCTGGGAGC TCCCAGAGGA AACTCTTGAC CACCAGTGGC TCCCTGAAGG GCTTTGTTA CCAAAGGTGG GGTAGGGACG GGGGTGGGAG TGGAGCGGAG GCCTTGTGTTT CCCGTGG			4193 4253 4313 4373 4433 4493 4553 4613 4650

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1203 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Met	Glu	Pro	Leu	Arg	His	Ser	Pro	Gly	Pro	Gly	Gly	Gln	Arg	Leu	Leu
1								10					15		
Leu	Pro	Ser	Met	Leu	Leu	Ala	Leu	Leu	Leu	Leu	Leu	Ala	Pro	Ser	Pro
			20				25					30			
Gly	His	Ala	Thr	Arg	Val	Val	Tyr	Lys	Val	Pro	Glu	Glu	Gln	Pro	Pro
							35		40			45			
Asn	Thr	Leu	Ile	Gly	Ser	Leu	Ala	Ala	Asp	Tyr	Gly	Phe	Pro	Asp	Val
							50		55			60			

Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr Leu Arg Val Asp
65 70 75 80

Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser Ile Asp Arg Glu
85 90 95

Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp Pro Cys Ile Leu
100 105 110

Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn Ala Ser Pro Arg
115 120 125

Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn Asp Asn Thr Pro
130 135 140

Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro Glu Asn Thr Asn
145 150 155 160

Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp Arg Asp Ala Gly
165 170 175

Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala Glu Asp Gln Glu
180 185 190

Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu Asp Arg Glu Arg
195 200 205

Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp Gly Ser Pro
210 215 220

Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val Leu Asp Thr Asn
225 230 235 240

Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu Ala Glu Leu Ser
245 250 255

Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val Lys Ala Asn Asp
260 265 270

Ser Asp Gln Gly Ala Asn Ala Glu Ile Glu Tyr Thr Phe His Gln Ala
275 280 285

Pro Glu Val Val Arg Arg Leu Leu Arg Leu Asp Arg Asn Thr Gly Leu
290 295 300

Ile Thr Val Gln Gly Pro Val Asp Arg Glu Asp Leu Ser Thr Leu Arg
305 310 315 320

Phe Ser Val Leu Ala Lys Asp Arg Gly Thr Asn Pro Lys Ser Ala Arg
325 330 335

Ala Gln Val Val Val Thr Val Lys Asp Met Asn Asp Asn Ala Pro Thr
340 345 350

Ile Glu Ile Arg Gly Ile Gly Leu Val Thr His Gln Asp Gly Met Ala
355 360 365

Asn Ile Ser Glu Asp Val Ala Glu Glu Thr Ala Val Ala Leu Val Gln
370 375 380

Val Ser Asp Arg Asp Glu Gly Glu Asn Ala Ala Val Thr Cys Val Val
385 390 395 400

Ala Gly Asp Val Pro Phe Gln Leu Arg Gln Ala Ser Glu Thr Gly Ser
405 410 415

Asp Ser Lys Lys Lys Tyr Phe Leu Gln Thr Thr Thr Pro Leu Asp Tyr
420 425 430

Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val Ala Val Asp Ser Gly
435 440 445

Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys Val Gln Val Val Asp
450 455 460

Val Asn Asp Asn Ala Pro Val Phe Thr Gln Ser Val Thr Glu Val Ala
465 470 475 480

Phe Pro Glu Asn Asn Lys Pro Gly Glu Val Ile Ala Glu Ile Thr Ala
485 490 495

Ser Asp Ala Asp Ser Gly Ser Asn Ala Glu Leu Val Tyr Ser Leu Glu
500 505 510

Pro Glu Pro Ala Ala Lys Gly Leu Phe Thr Ile Ser Pro Glu Thr Gly
515 520 525

Glu Ile Gln Val Lys Thr Ser Leu Asp Arg Glu Gln Arg Glu Ser Tyr
530 535 540

Glu Leu Lys Val Val Ala Ala Asp Arg Gly Ser Pro Ser Leu Gln Gly
545 550 555 560

Thr Ala Thr Val Leu Val Asn Val Leu Asp Cys Asn Asp Asn Asp Pro
565 570 575

Lys Phe Met Leu Ser Gly Tyr Asn Phe Ser Val Met Glu Asn Met Pro
580 585 590

Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp Gly Asp Lys Gly
595 600 605

Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp Asn Gly Asp Phe
610 615 620

Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser Leu Ser Phe Asp
625 630 635 640

Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys Ala Val Asp Gly
645 650 655

Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr Ile Asn Val Leu
660 665 670

Asp Glu Asn Asp Asn Ala Pro Tyr Ile Thr Ala Pro Ser Asn Thr Ser
675 680 685

His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu Thr Val Ser Gln
690 695 700

Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala Glu Leu Ile Tyr
705 710 715 720

Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln Ile Gly Ser His
725 730 735

Ser Gly Ala Ile Thr Leu Glu Lys Glu Ile Glu Arg Arg His His Gly
740 745 750

Leu His Arg Leu Val Val Lys Val Ser Asp Arg Gly Lys Pro Pro Arg
755 760 765

Tyr Gly Thr Ala Leu Val His Leu Tyr Val Asn Glu Thr Leu Ala Asn
770 775 780

Arg Thr Leu Leu Glu Thr Leu Leu Gly His Ser Leu Asp Thr Pro Leu
785 790 795 800

Asp Ile Asp Ile Ala Gly Asp Pro Glu Tyr Glu Arg Ser Lys Gln Arg
805 810 815

Gly Asn Ile Leu Phe Gly Val Val Ala Gly Val Val Ala Val Ala Leu
820 825 830

Leu Ile Ala Leu Ala Val Leu Val Arg Tyr Cys Arg Gln Arg Glu Ala
835 840 845

Lys Ser Gly Tyr Gln Ala Gly Lys Lys Glu Thr Lys Asp Leu Tyr Ala
850 855 860

Pro Lys Pro Ser Gly Lys Ala Ser Lys Gly Asn Lys Ser Lys Gly Lys
865 870 875 880

Lys Ser Lys Ser Pro Lys Pro Val Lys Pro Val Glu Asp Glu Asp Glu
885 890 895

Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met Ser Asp Ala Pro
900 905 910

Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr Pro Pro Gly Ser
915 920 925

Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro Leu Pro Ser Ile
930 935 940

Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys His Gln Val Val
945 950 955 960

Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr Gly Asp Thr Thr
965 970 975

Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr Arg Thr Asn Pro
980 985 990

Pro Lys Tyr Pro Ser Lys Gln Leu Pro His Arg Arg Val Thr Phe Ser
995 1000 1005

Ala Thr Ser Gln Ala Gln Glu Leu Gln Asp Pro Ser Gln His Ser Tyr
1010 1015 1020

Tyr Asp Ser Gly Leu Glu Glu Ser Glu Thr Pro Ser Ser Lys Ser Ser
1025 1030 1035 1040

Ser Gly Pro Arg Leu Gly Pro Leu Ala Leu Pro Glu Asp His Tyr Glu
1045 1050 1055

Arg Thr Thr Pro Asp Gly Ser Ile Gly Glu Met Glu His Pro Glu Asn
1060 1065 1070

-100-

Asp Leu Arg Pro Leu Pro Asp Val Ala Met Thr Gly Thr Cys Thr Arg
1075 1080 1085

Glu Cys Ser Glu Phe Gly His Ser Asp Thr Cys Trp Met Pro Gly Gln
1090 1095 1100

Ser Ser Pro Ser Arg Arg Thr Lys Ser Ser Ala Leu Lys Leu Ser Thr
1105 1110 1115 1120

Phe Met Pro Tyr Gln Asp Arg Gly Gly Gln Glu Pro Ala Gly Ala Gly
1125 1130 1135

Ser Pro Ser Pro Pro Glu Asp Arg Asn Thr Lys Thr Ala Pro Val Arg
1140 1145 1150

Leu Leu Pro Ser Tyr Ser Ala Phe Ser His Ser Ser His Asp Ser Cys
1155 1160 1165

Lys Asp Ser Ala Thr Leu Glu Glu Ile Pro Leu Thr Gln Thr Ser Asp
1170 1175 1180

Phe Pro Pro Ala Ala Thr Pro Ala Ser Ala Gln Thr Ala Lys Arg Glu
1185 1190 1195 1200

Ile Tyr Leu

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 115..2622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CGAAAGCCAT GTCGGACTCG TCGCCCAGCG CCCAAGCGCT AACCCGCTGA AAGTTTCTCA	60
GC G AAATCTC AGGGACGATC TG G ACCCCGC TGAGAGGAAC TGCTTTGAG TGAG ATG	117
Met 1	
.GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG	165
Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val	
5 10 15	
GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT	213
Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile	
20 25 30	
CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC	261
His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn	
35 40 45	

GTG GTC GCG AAC CTT GGT TTG GAT CTC GGT AGC CTC TCA GCC CGC AGG Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg Arg	309
50 55 60 65	
TTC CCG GTG GTG TCT GGA GCT AGC CGA AGA TTC TTT GAG GTG AAC CGG Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn Arg	357
70 75 80	
GAG ACC GGA GAG ATG TTT GTG AAC GAC CGT CTG GAT CGA GAG GAG CTG Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu Leu	405
85 90 95	
TGT GGG ACA CTG CCC TCT TGC ACT GTA ACT CTG GAG TTG GTA GTG GAG Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val Glu	453
100 105 110	
AAC CCG CTG GAG CTG TTC AGC GTG GAA GTG GTG ATC CAG GAC ATC AAC Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile Asn	501
115 120 125	
GAC AAC AAT CCT GCT TTC CCT ACC CAG GAA ATG AAA TTG GAG ATT AGC Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile Ser	549
130 135 140 145	
GAG GCC GTG GCT CCG GGG ACG CGC TTT CCG CTC GAG AGC GCG CAC GAT Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His Asp	597
150 155 160	
CCC GAT CTG GGA AGC AAC TCT TTA CAA ACC TAT GAG CTG AGC CGA AAT Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg Asn	645
165 170 175	
GAA TAC TTT GCG CTT CGC GTG CAG ACG CGG GAG GAC AGC ACC AAG TAC Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys Tyr	693
180 185 190	
GCG GAG CTG GTG TTG GAG CGC GCC CTG GAC CGA GAA CGG GAG CCT AGT Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro Ser	741
195 200 205	
CTC CAG TTA GTG CTG ACG GCG TTG GAC GGA GGG ACC CCA GCT CTC TCC Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu Ser	789
210 215 220 225	
GCC AGC CTG CCT ATT CAC ATC AAG GTG CTG GAC GCG AAT GAC AAT GCG Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn Ala	837
230 235 240	
CCT GTC TTC AAC CAG TCC TTG TAC CGG GCG CGC GTT CCT GGA GGA TGC Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly Cys	885
245 250 255	
ACC TCC GGC ACG CGC GTG GTA CAA GTC CTT GCA ACG GAT CTG GAT GAA Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp Glu	933
260 265 270	
GGC CCC AAC GGT GAA ATT ATT TAC TCC TTC GGC AGC CAC AAC CGC GCC Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg Ala	981
275 280 285	

GGC GTG CGG CAA CTA TTC GCC TTA GAC CTT GTA ACC GGG ATG CTG ACA Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu Thr 290 295 300 305	1029
ATC AAG GGT CGG CTG GAC TTC GAG GAC ACC AAA CTC CAT GAG ATT TAC Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr 310 315 320	1077
ATC CAG GCC AAA GAC AAG GGC GCC AAT CCC GAA GGA GCA CAT TGC AAA Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys 325 330 335	1125
GTG TTG GTG GAG GTT GTG GAT GTG AAT GAC AAC GCC CCG GAG ATC ACA Val Leu Val Glu Val Asp Val Asn Asp Asn Ala Pro Glu Ile Thr 340 345 350	1173
GTC ACC TCC GTG TAC AGC CCA GTA CCC GAG GAT GCC TCT GGG ACT GTC Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr Val 355 360 365	1221
ATC GCT TTG CTC AGT GTG ACT GAC CTG GAT GCT GGC GAG AAC GGG CTG Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly Leu 370 375 380 385	1269
GTG ACC TGC GAA GTT CCA CCG GGT CTC CCT TTC AGC CTT ACT TCT TCC Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser Ser 390 395 400	1317
CTC AAG AAT TAC TTC ACT TTG AAA ACC AGT GCA GAC CTG GAT CGG GAG Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg Glu 405 410 415	1365
ACT GTG CCA GAA TAC AAC CTC AGC ATC ACC GCC CGA GAC GCC GGA ACC Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly Thr 420 425 430	1413
CCT TCC CTC TCA GCC CTT ACA ATA GTG CGT GTT CAA GTG TCC GAC ATC Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp Ile 435 440 445	1461
AAT GAC AAC CCT CCA CAA TCT TCT CAA TCT TCC TAC GAC GTT TAC ATT Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr Ile 450 455 460 465	1509
GAA GAA AAC AAC CTC CCC GGG GCT CCA ATA CTA AAC CTA AGT GTC TGG Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val Trp 470 475 480	1557
GAC CCC GAC GCC CCG CAG AAT GCT CGG CTT TCT TTC TTT CTC TTG GAG Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu Glu 485 490 495	1605
CAA GGA GCT GAA ACC GGG CTA GTG GGT CGC TAT TTC ACA ATA AAT CGT Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn Arg 500 505 510	1653
GAC AAT GGC ATA GTG TCA TCC TTA GTG CCC CTA GAC TAT GAG GAT CGG Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp Arg 515 520 525	1701

CGG GAA TTT GAA TTA ACA GCT CAT ATC AGC GAT GGG GGC ACC CCG GTC Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro Val 530 535 540 545	1749
CTA GCC ACC AAC ATC AGC GTG AAC ATA TTT GTC ACT GAT CGC AAT GAC Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn Asp 550 555 560	1797
AAT GCC CCC CAG GTC CTA TAT CCT CGG CCA GGT GGG AGC TCG GTG GAG Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val Glu 565 570 575	1845
ATG CTG CCT CGA GGT ACC TCA GCT GGC CAC CTA GTG TCA CGG GTG GTA Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val Val 580 585 590	1893
GCG TGG GAC GCG GAT GCA GGG CAC AAT GCC TGG CTC TCC TAC AGT CTC Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser Leu 595 600 605	1941
TTT GGA TCC CCT AAC CAG AGC CTT TTT GCC ATA GGG CTG CAC ACT GGT Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr Gly 610 615 620 625	1989
CAA ATC AGT ACT GCC CGT CCA GTC CAA GAC ACA GAT TCA CCC AGG CAG Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg Gln 630 635 640	2037
ACT CTC ACT GTC TTG ATC AAA GAC AAT GGG GAG CCT TCG CTC TCC ACC Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser Thr 645 650 655	2085
ACT GCT ACC CTC ACT GTG TCA GTA ACC GAG GAC TCT CCT GAA GCC CGA Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala Arg 660 665 670	2133
GCC GAG TTC CCC TCT GGC TCT GCC CCC CGG GAG CAG AAA AAA AAT CTC Ala Glu Phe Pro Ser Gly Ser Ala Pro Arg Glu Gln Lys Lys Asn Leu 675 680 685	2181
ACC TTT TAT CTA CTT CTT TCT CTA ATC CTG GTT TCT GTG GGC TTC GTG Thr Phe Tyr Leu Leu Leu Ser Leu Ile Leu Val Ser Val Gly Phe Val 690 695 700 705	2229
GTC ACA GTG TTC GGA GTA ATC ATA TTC AAA GTT TAC AAG TGG AAG CAG Val Thr Val Phe Gly Val Ile Ile Phe Lys Val Tyr Lys Trp Lys Gln 710 715 720	2277
TCT AGA GAC CTA TAC CGA GCC CCG GTG AGC TCA CTG TAC CGA ACA CCA Ser Arg Asp Leu Tyr Arg Ala Pro Val Ser Ser Leu Tyr Arg Thr Pro 725 730 735	2325
GGG CCC TCC TTG CAC GCG GAC GCC GTG CGG GGA GGC CTG ATG TCG CCG Gly Pro Ser Leu His Ala Asp Ala Val Arg Gly Gly Leu Met Ser Pro 740 745 750	2373
CAC CTT TAC CAT CAG GTG TAT CTC ACC ACG GAC TCC CGC CGC AGC GAC His Leu Tyr His Gln Val Tyr Leu Thr Thr Asp Ser Arg Arg Ser Asp 755 760 765	2421

CCG CTG CTG AAG AAA CCT GGT GCA GCC AGT CCA CTG GCC AGC CGC CAG Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg Gln 770 775 780 785	2469
AAC ACG CTG CGG AGC TGT GAT CCG GTG TTC TAT AGG CAG GTG TTG GGT Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu Gly 790 795 800	2517
GCA GAG AGC GCC CCT CCC GGA CAG GTA AGG TTT AGC AAG TCA TGC TTG Ala Glu Ser Ala Pro Pro Gly Gln Val Arg Phe Ser Lys Ser Cys Leu 805 810 815	2565
ACC CTG TTA GTG CCT TTT TAT TCC TAC ATC ATA TTG AGA AGG CTG GAG Thr Leu Leu Val Pro Phe Tyr Ser Tyr Ile Ile Leu Arg Arg Leu Glu 820 825 830	2613
CTG TTT TTT TAGTGATGAA GATGTTTTC TGTTGATGCA TTCACACTTT Leu Phe Phe 835	2662
CAACTGGCTC TTCCTAGATC AAAGTTAGTG CCTTTGTGAG ATGGTGGCCT GCCAGAGTGT GGTTTGTGGT CCCATTTCAG GGGGAAGATA CTTGACTCAT CTGTGGACCT AATTCACATC CTCAGCG	2722 2782 2789

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 836 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val 1 5 10 15
Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val 20 25 30
Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly 35 40 45
Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg 50 55 60
Arg Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn 65 70 75 80
Arg Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu 85 90 95
Leu Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val 100 105 110
Glu Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile 115 120 125

Asn Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile
130 135 140

Ser Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His
145 150 155 160

Asp Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg
165 170 175

Asn Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys
180 185 190

Tyr Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro
195 200 205

Ser Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu
210 215 220

Ser Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn
225 230 235 240

Ala Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly
245 250 255

Cys Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp
260 265 270

Glu Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg
275 280 285

Ala Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu
290 295 300

Thr Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile
305 310 315 320

Tyr Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys
325 330 335

Lys Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile
340 345 350

Thr Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr
355 360 365

Val Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly
370 375 380

Leu Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser
385 390 395 400

Ser Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg
405 410 415

Glu Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly
420 425 430

Thr Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp
435 440 445

Ile Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr
450 455 460

Ile Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val
465 470 475 480

Trp Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu
485 490 495

Glu Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn
500 505 510

Arg Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp
515 520 525

Arg Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro
530 535 540

Val Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn
545 550 555 560

Asp Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val
565 570 575

Glu Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val
580 585 590

Val Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser
595 600 605

Leu Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr
610 615 620

Gly Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg
625 630 635 640

Gln Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser
645 650 655

Thr Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala
660 665 670

Arg Ala Glu Phe Pro Ser Gly Ser Ala Pro Arg Glu Gln Lys Lys Asn
675 680 685

Leu Thr Phe Tyr Leu Leu Leu Ser Leu Ile Leu Val Ser Val Gly Phe
690 695 700

Val Val Thr Val Phe Gly Val Ile Ile Phe Lys Val Tyr Lys Trp Lys
705 710 715 720

Gln Ser Arg Asp Leu Tyr Arg Ala Pro Val Ser Ser Leu Tyr Arg Thr
725 730 735

Pro Gly Pro Ser Leu His Ala Asp Ala Val Arg Gly Gly Leu Met Ser
740 745 750

Pro His Leu Tyr His Gln Val Tyr Leu Thr Thr Asp Ser Arg Arg Ser
755 760 765

Asp Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg
770 775 780

Gln Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu
785 790 795 800

Gly Ala Glu Ser Ala Pro Pro Gly Gln Val Arg Phe Ser Lys Ser Cys
805 810 815

Leu Thr Leu Leu Val Pro Phe Tyr Ser Tyr Ile Ile Leu Arg Arg Leu
 820 825 830

Glu Leu Phe Phe
835

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 115..2160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CGAAAGCCAT GTCGGACTCG TCGCCCAGCG CCCAAGCGCT AACCCGCTGA AAGTTTCTCA	60
GCGAAATCTC AGGGACGATC TGGACCCCGC TGAGAGGAAC TGCTTTGAG TGAG ATG Met 1	117
GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val 5 10 15	165
GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile 20 25 30	213
CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn 35 40 45	261
GTG GTC GCG AAC CTT GGT TTG GAT CTC GGT AGC CTC TCA GCC CGC AGG Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg Arg 50 55 60 65	309
TTC CCG GTG GTG TCT GGA GCT AGC CGA AGA TTC TTT GAG GTG AAC CGG Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn Arg 70 75 80	357
GAG ACC GGA GAG ATG TTT GTG AAC GAC CGT CTG GAT CGA GAG GAG CTG Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu Leu 85 90 95	405
TGT GGG ACA CTG CCC TCT TGC ACT GTA ACT CTG GAG TTG GTA GTG GAG Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val Glu 100 105 110	453

AAC CCG CTG GAG CTG TTC AGC GTG GAA GTG GTG ATC CAG GAC ATC AAC Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile Asn 115 120 125	501
GAC AAC AAT CCT GCT TTC CCT ACC CAG GAA ATG AAA TTG GAG ATT AGC Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile Ser 130 135 140 145	549
GAG GCC GTG GCT CCG GGG ACG CGC TTT CCG CTC GAG AGC GCG CAC GAT Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His Asp 150 155 160	597
CCC GAT CTG GGA AGC AAC TCT TTA CAA ACC TAT GAG CTG AGC CGA AAT Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg Asn 165 170 175	645
GAA TAC TTT GCG CTT CGC GTG CAG ACG CGG GAG GAC AGC ACC AAG TAC Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys Tyr 180 185 190	693
GCG GAG CTG GTG TTG GAG CGC GCC CTG GAC CGA GAA CGG GAG CCT AGT Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro Ser 195 200 205	741
CTC CAG TTA GTG CTG ACG GCG TTG GAC GGA GGG ACC CCA GCT CTC TCC Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu Ser 210 215 220 225	789
GCC AGC CTG CCT ATT CAC ATC AAG GTG CTG GAC GCG AAT GAC AAT GCG Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn Ala 230 235 240	837
CCT GTC TTC AAC CAG TCC TTG TAC CGG GCG CGC GTT CCT GGA GGA TGC Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly Cys 245 250 255	885
ACC TCC GGC ACG CGC GTG GTA CAA GTC CTT GCA ACG GAT CTG GAT GAA Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp Glu 260 265 270	933
GGC CCC AAC GGT GAA ATT ATT TAC TCC TTC GGC AGC CAC AAC CGC GCC Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg Ala 275 280 285	981
GGC GTG CGG CAA CTA TTC GCC TTA GAC CTT GTA ACC GGG ATG CTG ACA Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu Thr 290 295 300 305	1029
ATC AAG GGT CGG CTG GAC TTC GAG GAC ACC AAA CTC CAT GAG ATT TAC Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr 310 315 320	1077
ATC CAG GCC AAA GAC AAG GGC GCC AAT CCC GAA GGA GCA CAT TGC AAA Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys 325 330 335	1125
GTG TTG GTG GAG GTT GTG GAT GTG AAT GAC AAC GCC CCG GAG ATC ACA Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile Thr 340 345 350	1173

GTC ACC TCC GTG TAC AGC CCA GTA CCC GAG GAT GCC TCT GGG ACT GTC	1221
Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr Val	
355 360 365	
ATC GCT TTG CTC AGT GTG ACT GAC CTG GAT GCT GGC GAG AAC GGG CTG	1269
Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly Leu	
370 375 380 385	
GTG ACC TGC GAA GTT CCA CCG GGT CTC CCT TTC AGC CTT ACT TCT TCC	1317
Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser Ser	
390 395 400	
CTC AAG AAT TAC TTC ACT TTG AAA ACC AGT GCA GAC CTG GAT CGG GAG	1365
Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg Glu	
405 410 415	
ACT GTG CCA GAA TAC AAC CTC AGC ATC ACC GCC CGA GAC GCC GGA ACC	1413
Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly Thr	
420 425 430	
CCT TCC CTC TCA GCC CTT ACA ATA GTG CGT GTT CAA GTG TCC GAC ATC	1461
Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp Ile	
435 440 445	
AAT GAC AAC CCT CCA CAA TCT TCT CAA TCT TCC TAC GAC GTT TAC ATT	1509
Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr Ile	
450 455 460 465	
GAA GAA AAC AAC CTC CCC GGG GCT CCA ATA CTA AAC CTA AGT GTC TGG	1557
Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val Trp	
470 475 480	
GAC CCC GAC GCC CCG CAG AAT GCT CGG CTT TCT TTC TTT CTC TTG GAG	1605
Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu Glu	
485 490 495	
CAA GGA GCT GAA ACC GGG CTA GTG GGT CGC TAT TTC ACA ATA AAT CGT	1653
Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn Arg	
500 505 510	
GAC AAT GGC ATA GTG TCA TCC TTA GTG CCC CTA GAC TAT GAG GAT CGG	1701
Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp Arg	
515 520 525	
CGG GAA TTT GAA TTA ACA GCT CAT ATC AGC GAT GGG GGC ACC CCG GTC	1749
Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro Val	
530 535 540 545	
CTA GCC ACC AAC ATC AGC GTG AAC ATA TTT GTC ACT GAT CGC AAT GAC	1797
Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn Asp	
550 555 560	
AAT GCC CCC CAG GTC CTA TAT CCT CGG CCA GGT GGG AGC TCG GTG GAG	1845
Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val Glu	
565 570 575	
ATG CTG CCT CGA GGT ACC TCA GCT GGC CAC CTA GTG TCA CGG GTG GTA	1893
Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val Val	
580 585 590	

GGC TGG GAC GCG GAT GCA GGG CAC AAT GCC TGG CTC TCC TAC AGT CTC Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser Leu 595 600 605	1941
TTT GGA TCC CCT AAC CAG AGC CTT TTT GCC ATA GGG CTG CAC ACT GGT Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr Gly 610 615 620 625	1989
CAA ATC AGT ACT GCC CGT CCA GTC CAA GAC ACA GAT TCA CCC AGG CAG Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg Gln 630 635 640	2037
ACT CTC ACT GTC TTG ATC AAA GAC AAT GGG GAG CCT TCG CTC TCC ACC Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser Thr 645 650 655	2085
ACT GCT ACC CTC ACT GTG TCA GTA ACC GAG GAC TCT CCT GAA GCC CGA Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala Arg 660 665 670	2133
GCC GAG TTC CCC TCT GGC TCT GCC AGT TAAACCTTCT TTAATTATGG Ala Glu Phe Pro Ser Gly Ser Ala Ser 675 680	2180
ATAGCCATT AACATTTTG AACAGTGGAC CATTAAACCT CGGCCTACCC CCTCCAAC TG TCCTGGTGTAT GAGTCATTA GCTAAGTTAA ATTAAATTGAA CTTTGATCTA AACCAAAACA AATCAGGAAA ATAAAGCTGT AAAGGAAC TT CAAGCATT CCAAAACCAA CTAGAAATT CTTGAAGTTT CGAGTGAGCA TTGCCTGTGC CAGTATTCTT CATTATAGGA TTATAAACTC GTTTTTTTCC CAAAGCGCAT GTCTACGCCA GGCAGAGGAG TAATTATTCA GCCAATT TGGATGTAAC GATGGATATA AATAATTGAT AGCACCTAGA GGCTTCCAGT TTGGGTGGAA GGCTAAAAGT AGAGGGGAAC TCACTCACTT GAGAAATGAT ATTAAAGTGA ATAAATAGTT CTCTTCTATG AACTATTAC TATTTAGTTC TCTGGAAAAC TTAAGTGTAT TAATGATTAG AACATCAAAT CCTAAGTAAA GAAATGACAT TTTAAATATA AAAAGCCAAA CTTTAAATAA ATCATAGAGA CCTCAGACAT AATATAGGAA A	2240 2300 2360 2420 2480 2540 2600 2660 2720 2751

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 682 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val
1 5 10 15

Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val
20 25 30

Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly
35 40 45

Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg
50 55 60

Arg Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn
65 70 75 80

Arg Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu
85 90 95

Leu Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val
100 105 110

Glu Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile
115 120 125

Asn Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile
130 135 140

Ser Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His
145 150 155 160

Asp Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg
165 170 175

Asn Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys
180 185 190

Tyr Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro
195 200 205

Ser Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu
210 215 220

Ser Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn
225 230 235 240

Ala Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly
245 250 255

Cys Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp
260 265 270

Glu Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg
275 280 285

Ala Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu
290 295 300

Thr Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile
305 310 315 320

Tyr Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys
325 330 335

Lys Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile
340 345 350

Thr Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr
355 360 365

Val Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly
370 375 380

Leu Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser
385 390 395 400

Ser Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg
405 410 415

Glu Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly
420 425 430

Thr Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp
435 440 445

Ile Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr
450 455 460

Ile Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val
465 470 475 480

Trp Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu
485 490 495

Glu Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn
500 505 510

Arg Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp
515 520 525

Arg Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro
530 535 540

Val Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn
545 550 555 560

Asp Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val
565 570 575

Glu Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val
580 585 590

Val Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser
595 600 605

Leu Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr
610 615 620

Gly Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg
625 630 635 640

Gln Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser
645 650 655

Thr Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala
660 665 670

Arg Ala Glu Phe Pro Ser Gly Ser Ala Ser
675 680

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAATTCGGCA CGAGGCTGAA CTGAGGGTGA CGGACATAAA CGACTATTCT CCAGTGTCA	60
GTGAAAGAGA AATGATACTG AGGATACCAG AAAACAGTGC TCGGGGAAAT ACATTCCTT	120
TAAACAATGC TCTGGACTCA GACGTAGATA TCAACAATAT CCAGACCTAT AGGCTCAGCT	180
CAAACCTCTCA TTTCTGGTT GTAACCCGCA ACCGCAGTGA TGGCAGGAAG TACCCAGAGC	240
TGGTGCTGGA GAAAGAACTG GATCGAGAGG AGGAACCTGA GCTGAGGTTA ACGCTGACAG	300
CTTTGGATGG TGGCTCTCCT CCCCGGTCTG GGACGACACA GGTCTCTATT GAAGTAGTGG	360
ACACCAACGA TAATGCACCC GAGTTTCAGC AGCCAACATA CCAAGTGCAA ACTCCCGAGA	420
ACAGTCCCAC CGGCTCTCTG GTACTCACAG TCTCAGCCAA TGACTTAGAC AGTGGAGACT	480
ATGGGAAAGT CTTGTACGCA CTTTCGCAAC CCTCAGAAGA TATTAGCAAA ACATTCGAGG	540
TAAACCCCTGT AACCGGGGAA ATTGCGCTAC GAAAAGAGGT GAATTTTGAA ACTATTCTT	600
CGTATGAAGT GGTTATCAAG GGGACGGACG GGGGAGGTCT CTCAGGAAAA TGCACTCTGT	660
TACTGCAGGT GGTGGACGTG AATGACAATG CCCCAGAAAGT GATGCTATCT GCGCTAACCA	720
ACCCAGTCCC AGAAAATTCC CCCGATGAGG TAGTGGCTGT TTTCACTGTT AGAGATCCTG	780
ACTCTGGAA CAACGGAAAA GTGATTGCAT CCATCGAGGA AGACCTGCC 3' TTTCTTCTAA	840
AATCTTCAGG AAAGAACTTT TACACTTAG TAACCAAGGG AGCACTTGAC AGGGAAGAAA	900
GAGAGCAATT GAACATCACC ATCACAGTCA CTGACCTGGG CATAACCCAGG CTCACCACCC	960
AACACACCAT AACAGTGCAG GTGGCAGACA TCAACGACAA TGCCCCCTCC TTCACCCAAA	1020
CCTCCTACAC CATGTTTGTCA CGCGAGAACCA ACAGCCCCGC CCTGCACATA GGCACCATCA	1080
GCGCCACAGA CTCAGACTCA GGATCCAATG CCCACATCAC CTACTCGCTG CTACCGCCCC	1140
AAGACCCACA GCTGGCCCTC GACTCGCTCA TCTCCATCAA TGTAGACAAC GGGCAGCTGT	1200
TCGCGCTCAG GGCGCTAGAC TATGAGGCTC TGCAGGGCTT CGAGTTCCAT GTGGCGCCA	1260
CAGACCAAGG CTCGCCCCGC CTCAGCAGCC AGGCTCTGGT GCACGTGGTG GTGTTGGACG	1320
ACAATGACAA TGCACCCCTTC GTGCTCTACC CGCTGCAAAA CGCCTCTGCA CCCTTCACTG	1380
AGCTGCTGCC CAGGGCGGCA GAGCCTGGAT ACCTGGTTAC CAAGGTGGTA GCTGTGGACC	1440
GCGACTCTGG CCAGAATGCC TGGCTGTCA TCCAGCTGCT CAAGGCCACG GAGCCCGGGC	1500

TGTTCAACGT ATGGGCGCAC AATGGCGAGG TACGCACCTC CAGGCTGCTG AGCGAGCGCG	1560
ACGCACCCAA GCACAAGCTG CTGCTGTTGG TCAAGGACAA TGGAGATCCT CCACGCTCTG	1620
CCAGTGTAC TCTGCACGTG CTAGTGGTGG ATGCCTCTC TCAGCCCTAC CTGCCTCTGC	1680
CAGAGGTGGC GCACGACCCCT GCACAAGAAG AAGATGCGCT AACACTCTAC CTGGTCATAG	1740
CTTTGGCATC TGTGTCTTCT CTCTTCCTCT TGTCTGTGCT GCTGTTCGTG GGGGTGAGGC	1800
TCTGCAGGAG GGCCAGGGCA GCCTCTCTGA GTGCCTATTTC TGTGCCTGAA GGCCACTTTC	1860
CTGGCCAGCT GGTGGATGTC AGAGGTATGG GGACCTGTC CCAGAGCTAC CAGTATGATG	1920
TATGTCTGAT GGGGGATTCT TCTGGGACCA GCGAATTAA CTTCTTAAAG CCAGTTCTGC	1980
CTAGCTCTCT GCACCAGTGC TCTGGGAAAG AAATAGAGGA AAATTCCACA CTCCAGAATA	2040
GTTTGGGTT TCATCATTAA TAGAAAACTA CTTTACAGAT ATTTAATTCC AAATATCATC	2100
TTGTTGATTA ACTAAAGTCT GTTCACATGT AGCTAGCTAG CAACGATTTC AATGTTCACT	2160
TTACCCATCT TTTTCAGGG TCATGTCTAA AGCTACAAGT TTGNCTTTAC TTATACTTGT	2220
CGCACAGAAT NNNNNNNNNN TGGTGTATAA GTCACAGTCA TGGGATACTG GCACAAGATG	2280
GCAGCTTGAT TGCTCAGTTA TGGCTGCAA GGGNGCTTG AGTTTAGGGA ATGTGTTAGA	2340
GCTGGAATAA GTTTCTGAG AAATGTGTAA GACAAATTTC TTTGCACAT TCCCTGTGTT	2400
CCTGTACCCC TGTTCCAGA ACTACGAAAT GTGTCATCAG AAGGCATGCT CACATTTC	2460
CCTTTGTTG CGTGACCCGG GTGCCAGAAA TTAAATAAAA TTAGCATGGA GTTCAATGCA	2520
GCATTAACAA AAAGTTACTT CTACAAACCT TTTATTCGAC GGTTAAAATT GTAACTTCCC	2580
ACCCATGAG GCTGGCTGTA AGAACCAAGTA TGAATGGGTG TCTATCGCAA CCTTATTTC	2640
AAAAATCAAA CAAAAGGAGA AATGAGAGAC CAAACAACAC GCTACAGGAA AGATTTCAT	2700
AGGATGTATG TATGGACACA AAAACTGGGA TACAGACATT TTAAATCTGT TGGTACCA	2760
TGGTGGCGCT GCAGGCTAAA GAAATGCAAG GGAAATTAAA AAGAGGCTGA GCTAGAAGTC	2820
AAAAAAAAAA A	2831

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 763..3123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTATTTTCC ACAGTTAAA ATTTCATAA AATCATAACT CTCTGACTTT ATGTAGAAAG	60
GATACCACAC TGGAATTAAC GTGTAGCTTT TTCTTGATGT AATCCAACCA ATGGGAGCAC	120
AATTCTGGTA CATAGGCTGT CTAGAATTG AAAGAAATTA AAGAATTCA TTTGTTTGC	180
TGATAAATT TTAAGAAATC ACGTGGCTTT ATGTTATTAT TATTACAAGA TGACTGATCA	240
CTATTATGTC TTCTTCACT TCTCAATTTC CCTCAGAACCA CTACACCCAG ACTACAGGCT	300
CTGGAGGGTG GGGACCATGT CTGGGTTGTT TACTGATGTA TTTCATAATT TGGCACATAG	360
AGACCAATAA TACTCCTTTA AATGAAGAAA TTAATAATT CCATTGCGTG ATATTGTGAT	420
TACATCATT CCTCCCAATT TCCAAACTCC TAATAGAATA GAGAATAGAT CAATTGTAGC	480
AATTCTGTTT GCAGCAAAGA CAACGCATGG TGGCGCTGCA GGCTAAGGCT TCAAAAAAAG	540
GAAAAGGAAA AAGCCCATGA AATGCTACTA GCTACTTCAG ACCTCTTCA GCCTAAGAGG	600
AAAGCCTGTT AGCAGAGCAC GGACCAAGTGT CTCCGGAGAA TGCTATTCTC CTACATTCC	660
GAACAGGTTA TCAACGCACA GATCGATCAC TGCCTCTGTC CCATCGCTCC CTGAAGTAGC	720
TCTGACTCCG GTTCCTTGAA AGGGGCAGTGT ACAGAAGTAA AG ATG GAG CCT GCA	774
Met Glu Pro Ala	
1	
GGG GAG CGC TTT CCC GAA CAA AGG CAA GTC CTG ATT CTC CTT CTT TTA	822
Gly Glu Arg Phe Pro Glu Gln Arg Gln Val Leu Ile Leu Leu Leu Leu	
5 10 15 20	
CTG GAA GTG ACT CTG GCA GGC TGG GAA CCC CGT CGC TAT TCT GTG ATG	870
Leu Glu Val Thr Leu Ala Gly Trp Glu Pro Arg Arg Tyr Ser Val Met	
25 30 35	
GAG GAA ACA GAG AGA GGT TCT TTT GTA GCC AAC CTG GCC AAT GAC CTA	918
Glu Glu Thr Glu Arg Gly Ser Phe Val Ala Asn Leu Ala Asn Asp Leu	
40 45 50	
GGG CTG GGA GTG GGG GAG CTA GCC GAG CGG GGA GCC CGG GTA GTT TCT	966
Gly Leu Gly Val Gly Glu Leu Ala Glu Arg Gly Ala Arg Val Val Ser	
55 60 65	
GAG GAT AAC GAA CAA GGC TTG CAG CTT GAT CTG CAG ACC GGG CAG TTG	1014
Glu Asp Asn Glu Gln Gly Leu Gln Leu Asp Leu Gln Thr Gly Gln Leu	
70 75 80	
ATA TTA AAT GAG AAG CTG GAC CGG GAG AAG CTG TGT GGC CCT ACT GAG	1062
Ile Leu Asn Glu Lys Leu Asp Arg Glu Lys Leu Cys Gly Pro Thr Glu	
85 90 95 100	
CCC TGT ATA ATG CAT TTC CAA GTG TTA CTG AAA AAA CCT TTG GAA GTA	1110
Pro Cys Ile Met His Phe Gln Val Leu Leu Lys Lys Pro Leu Glu Val	
105 110 115	

TTT CGA GCT GAA CTA CTA GTG ACA GAC ATA AAC GAT CAT TCT CCT GAG Phe Arg Ala Glu Leu Leu Val Thr Asp Ile Asn Asp His Ser Pro Glu 120 125 130	1158
TTT CCT GAA AGA GAA ATG ACC CTG AAA ATC CCA GAA ACT AGC TCC CTT Phe Pro Glu Arg Glu Met Thr Leu Lys Ile Pro Glu Thr Ser Ser Leu 135 140 145	1206
GGG ACT GTG TTT CCT CTG AAA AAA GCT CGG GAC TTG GAC GTG GGC AGC Gly Thr Val Phe Pro Leu Lys Lys Ala Arg Asp Leu Asp Val Gly Ser 150 155 160	1254
AAT AAT GTT CAA AAC TAC AAT ATT TCT CCC AAT TCT CAT TTC CAT GTT Asn Asn Val Gln Asn Tyr Asn Ile Ser Pro Asn Ser His Phe His Val 165 170 175 180	1302
TCC ACT CGC ACC CGA GGG GAT GGC AGG AAA TAC CCA GAG CTG GTG CTG Ser Thr Arg Thr Arg Gly Asp Gly Arg Lys Tyr Pro Glu Leu Val Leu 185 190 195	1350
GAC ACA GAA CTG GAT CGC GAG GAG CAG GCC GAG CTC AGA TTA ACC TTG Asp Thr Glu Leu Asp Arg Glu Glu Gln Ala Glu Leu Arg Leu Thr Leu 200 205 210	1398
ACA GCG GTG GAC GGT GGC TCT CCA CCC CGA TCT GGC ACC GTC CAG ATC Thr Ala Val Asp Gly Ser Pro Pro Arg Ser Gly Thr Val Gln Ile 215 220 225	1446
CTC ATC TTG GTC TTG GAC GCC AAT GAC AAT GCC CCG GAG TTT GTG CAG Leu Ile Leu Val Leu Asp Ala Asn Asp Asn Ala Pro Glu Phe Val Gln 230 235 240	1494
GCG CTC TAC GAG GTG CAG GTC CCA GAG AAC AGC CCA GTA GGC TCC CTA Ala Leu Tyr Glu Val Gln Val Pro Glu Asn Ser Pro Val Gly Ser Leu 245 250 255 260	1542
GTT GTC AAG GTC TCT GCT AGG GAT TTA GAC ACT GGG ACA AAT GGA GAG Val Val Lys Val Ser Ala Arg Asp Leu Asp Thr Gly Thr Asn Gly Glu 265 270 275	1590
ATA TCA TAC TCC CTT TAT TAC AGC TCT CAG GAG ATA GAC AAA CCT TTT Ile Ser Tyr Ser Leu Tyr Tyr Ser Ser Gln Glu Ile Asp Lys Pro Phe 280 285 290	1638
GAG CTA AGC AGC CTT TCA GGA GAA ATT CGA CTA ATT AAA AAA CTA GAT Glu Leu Ser Ser Leu Ser Gly Glu Ile Arg Leu Ile Lys Lys Leu Asp 295 300 305	1686
TTT GAG ACA ATG TCT TCA TAT GAT CTA GAT ATA GAG GCA TCT GAT GGC Phe Glu Thr Met Ser Ser Tyr Asp Leu Asp Ile Glu Ala Ser Asp Gly 310 315 320	1734
GGG GGA CTT TCT GGA AAA TGC TCT GTC TCT GTT AAG GTG CTG GAT GTT Gly Gly Leu Ser Gly Lys Cys Ser Val Ser Val Lys Val Leu Asp Val 325 330 335 340	1782
AAC GAT AAC TTC CCG GAA CTA AGT ATT TCA TCA CTT ACC AGC CCT ATT Asn Asp Asn Phe Pro Glu Leu Ser Ile Ser Ser Leu Thr Ser Pro Ile 345 350 355	1830

CCC GAG AAT TCT CCA GAG ACA GAA GTG GCC CTG TTT AGG ATT AGA GAC Pro Glu Asn Ser Pro Glu Thr Glu Val Ala Leu Phe Arg Ile Arg Asp 360 365 370	1878
CGA GAC TCT GGA GAA AAT GGA AAA ATG ATT TGC TCA ATT CAG GAT GAT Arg Asp Ser Gly Glu Asn Gly Lys Met Ile Cys Ser Ile Gln Asp Asp 375 380 385	1926
GTT CCT TTT AAG CTA AAA CCT TCT GTT GAG AAT TTC TAC AGG CTG GTA Val Pro Phe Lys Leu Lys Pro Ser Val Glu Asn Phe Tyr Arg Leu Val 390 395 400	1974
ACA GAA GGG GCG CTG GAC AGA GAG ACC AGA GCC GAG TAC AAC ATC ACC Thr Glu Gly Ala Leu Asp Arg Glu Thr Arg Ala Glu Tyr Asn Ile Thr 405 410 415 420	2022
ATC ACC ATC ACA GAC TTG GGG ACT CCA AGG CTG AAA ACC GAG CAG AGC Ile Thr Ile Thr Asp Leu Gly Thr Pro Arg Leu Lys Thr Glu Gln Ser 425 430 435	2070
ATA ACC GTG CTG GTG TCG GAC GTC AAT GAC AAC GCC CCC GCC TTC ACC Ile Thr Val Leu Val Ser Asp Val Asn Asp Asn Ala Pro Ala Phe Thr 440 445 450	2118
CAA ACC TCC TAC ACC CTG TTC GTC CGC GAG AAC AAC AGC CCC GCC CTG Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser Pro Ala Leu 455 460 465	2166
CAC ATC GGC AGT GTC AGC GCC ACA GAC AGA GAC TCG GGC ACC AAC GCC His Ile Gly Ser Val Ser Ala Thr Asp Arg Asp Ser Gly Thr Asn Ala 470 475 480	2214
CAG GTC ACC TAC TCG CTG CTG CCG CCC CAG GAC CCG CAC CTG CCC CTA Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp Pro His Leu Pro Leu 485 490 495 500	2262
ACC TCC CTG GTC TCC ATT AAC ACG GAC AAC GGC CAC CTG TTC GCT CTC Thr Ser Leu Val Ser Ile Asn Thr Asp Asn Gly His Leu Phe Ala Leu 505 510 515	2310
CAG TCG CTG GAC TAC GAG GCC CTG CAG GCT TTC GAG TTC CGC GTG GGC Gln Ser Leu Asp Tyr Glu Ala Leu Gln Ala Phe Glu Phe Arg Val Gly 520 525 530	2358
GCC ACA GAC CGC GGC TTC CCG GCG CTG AGC AGC GAG GCG CTG GTG CGA Ala Thr Asp Arg Gly Phe Pro Ala Leu Ser Ser Glu Ala Leu Val Arg 535 540 545	2406
GTG CTG GTG CTG GAC GCC AAC GAC AAC TCG CCC TTC GTG CTG TAC CCG Val Leu Val Leu Asp Ala Asn Asp Asn Ser Pro Phe Val Leu Tyr Pro 550 555 560	2454
CTG CAG AAC GGC TCC GCG CCC TGC ACC GAG CTG GTG CCC CGG GCG GCC Leu Gln Asn Gly Ser Ala Pro Cys Thr Glu Leu Val Pro Arg Ala Ala 565 570 575 580	2502
GAG CCG GGC TAC CTG GTG ACC AAG GTG GTG GCG GTG GAC GGC GAC TCG Glu Pro Gly Tyr Leu Val Thr Lys Val Val Ala Val Asp Gly Asp Ser 585 590 595	2550

GGC CAG AAC GCC TGG CTG TCG TAC CAG CTG CTC AAG GCC ACG GAG CCC Gly Gln Asn Ala Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Pro 600 605 610	2598
GGG CTG TTC GGC GTG TGG GCG CAC AAT GGC GAG GTG CGC ACC GCC AGG Gly Leu Phe Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg 615 620 625	2646
CTG CTG AGC GAG CGC GAC GTG GCC AAG CAC AGG CTA GTG GTG CTG GTC Leu Leu Ser Glu Arg Asp Val Ala Lys His Arg Leu Val Val Leu Val 630 635 640	2694
AAG GAC AAT GGC GAG CCT CCG CGC TCG GCC ACA GCC ACG CTG CAA GTG Lys Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu Gln Val 645 650 655 660	2742
CTC CTG GTG GAC GGC TTC TCT CAG CCC TAC CTG CCG CTC CCA GAG GCG Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu Ala 665 670 675	2790
GCC CCG GCC CAA GCC CAG GCC GAC TCG CTT ACC GTC TAC CTG GTG GTG Ala Pro Ala Gln Ala Gln Asp Ser Leu Thr Val Tyr Leu Val Val 680 685 690	2838
GCA TTG GCC TCG GTG TCT TCG CTC TTC CTC TTC TCG GTG TTC CTG TTC Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val Phe Leu Phe 695 700 705	2886
GTG GCA GTG CGG CTG TGC AGG AGG AGC AGG GCG GCC TCA GTG GGT CGC Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala Ser Val Gly Arg 710 715 720	2934
TGC TCG GTG CCC GAG GGC CCC TTT CCA GGG CAT CTG GTG GAC GTG AGC Cys Ser Val Pro Glu Gly Pro Phe Pro Gly His Leu Val Asp Val Ser 725 730 735 740	2982
GGC ACC GGG ACC CTT TCC CAG AGC TAC CAG TAC GAG GTG TGT CTG ACG Gly Thr Gly Thr Leu Ser Gln Ser Tyr Gln Tyr Glu Val Cys Leu Thr 745 750 755	3030
GGA GGC TCT GAA AGT AAT GAT TTC AAG TTC TTG AAG CCT ATA TTC CCA Gly Gly Ser Glu Ser Asn Asp Phe Lys Phe Leu Lys Pro Ile Phe Pro 760 765 770	3078
AAT ATT GTA AGC CAG GAC TCT AGG AGG AAA TCA GAA TTT CTA GAA Asn Ile Val Ser Gln Asp Ser Arg Arg Lys Ser Glu Phe Leu Glu 775 780 785	3123
TAATGTAGGT ATCTGTAGCT TTCCGACCGT CTGTTAATT TGTCTTCCTC ACTTTTCACC	3183
TTAGTTTTTT TTAACCCCTT AGTAATCTTG AATTCTACTT TTTTTAAAT TTCTACTGTT	3243
GTCTTTAGTA ATGTTACTCA TTTCCTTGT CTGATTGTTA GTTTCAAT TATGTATTA	3303
TTATAAATAT TTTATATCAG GAAAGTTCAT ATTTCTGAAT AAATTAATAG	3353

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Glu Pro Ala Gly Glu Arg Phe Pro Glu Gln Arg Gln Val Leu Ile
1 5 10 15

Leu Leu Leu Leu Leu Glu Val Thr Leu Ala Gly Trp Glu Pro Arg Arg
20 25 30

Tyr Ser Val Met Glu Glu Thr Glu Arg Gly Ser Phe Val Ala Asn Leu
35 40 45

Ala Asn Asp Leu Gly Leu Gly Val Gly Glu Leu Ala Glu Arg Gly Ala
50 55 60

Arg Val Val Ser Glu Asp Asn Glu Gln Gly Leu Gln Leu Asp Leu Gln
65 70 75 80

Thr Gly Gln Leu Ile Leu Asn Glu Lys Leu Asp Arg Glu Lys Leu Cys
85 90 95

Gly Pro Thr Glu Pro Cys Ile Met His Phe Gln Val Leu Lys Lys
100 105 110

Pro Leu Glu Val Phe Arg Ala Glu Leu Leu Val Thr Asp Ile Asn Asp
115 120 125

His Ser Pro Glu Phe Pro Glu Arg Glu Met Thr Leu Lys Ile Pro Glu
130 135 140

Thr Ser Ser Leu Gly Thr Val Phe Pro Leu Lys Lys Ala Arg Asp Leu
145 150 155 160

Asp Val Gly Ser Asn Asn Val Gln Asn Tyr Asn Ile Ser Pro Asn Ser
165 170 175

His Phe His Val Ser Thr Arg Thr Arg Gly Asp Gly Arg Lys Tyr Pro
180 185 190

Glu Leu Val Leu Asp Thr Glu Leu Asp Arg Glu Glu Gln Ala Glu Leu
195 200 205

Arg Leu Thr Leu Thr Ala Val Asp Gly Gly Ser Pro Pro Arg Ser Gly
210 215 220

Thr Val Gln Ile Leu Ile Leu Val Leu Asp Ala Asn Asp Asn Ala Pro
225 230 235 240

Glu Phe Val Gln Ala Leu Tyr Glu Val Gln Val Pro Glu Asn Ser Pro
245 250 255

Val Gly Ser Leu Val Val Lys Val Ser Ala Arg Asp Leu Asp Thr Gly
260 265 270

Thr Asn Gly Glu Ile Ser Tyr Ser Leu Tyr Tyr Ser Ser Gln Glu Ile
275 280 285

Asp Lys Pro Phe Glu Leu Ser Ser Leu Ser Gly Glu Ile Arg Leu Ile
290 295 300

Lys Lys Leu Asp Phe Glu Thr Met Ser Ser Tyr Asp Leu Asp Ile Glu
305 310 315 320

Ala Ser Asp Gly Gly Gly Leu Ser Gly Lys Cys Ser Val Ser Val Lys
325 330 335

Val Leu Asp Val Asn Asp Asn Phe Pro Glu Leu Ser Ile Ser Ser Leu
340 345 350

Thr Ser Pro Ile Pro Glu Asn Ser Pro Glu Thr Glu Val Ala Leu Phe
355 360 365

Arg Ile Arg Asp Arg Asp Ser Gly Glu Asn Gly Lys Met Ile Cys Ser
370 375 380

Ile Gln Asp Asp Val Pro Phe Lys Leu Lys Pro Ser Val Glu Asn Phe
385 390 395 400

Tyr Arg Leu Val Thr Glu Gly Ala Leu Asp Arg Glu Thr Arg Ala Glu
405 410 415

Tyr Asn Ile Thr Ile Thr Asp Leu Gly Thr Pro Arg Leu Lys
420 425 430

Thr Glu Gln Ser Ile Thr Val Leu Val Ser Asp Val Asn Asp Asn Ala
435 440 445

Pro Ala Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn
450 455 460

Ser Pro Ala Leu His Ile Gly Ser Val Ser Ala Thr Asp Arg Asp Ser
465 470 475 480

Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp Pro
485 490 495

His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Thr Asp Asn Gly His
500 505 510

Leu Phe Ala Leu Gln Ser Leu Asp Tyr Glu Ala Leu Gln Ala Phe Glu
515 520 525

Phe Arg Val Gly Ala Thr Asp Arg Gly Phe Pro Ala Leu Ser Ser Glu
530 535 540

Ala Leu Val Arg Val Leu Val Leu Asp Ala Asn Asp Asn Ser Pro Phe
545 550 555 560

Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala Pro Cys Thr Glu Leu Val
565 570 575

Pro Arg Ala Ala Glu Pro Gly Tyr Leu Val Thr Lys Val Val Ala Val
580 585 590

Asp Gly Asp Ser Gly Gln Asn Ala Trp Leu Ser Tyr Gln Leu Leu Lys
595 600 605

Ala Thr Glu Pro Gly Leu Phe Gly Val Trp Ala His Asn Gly Glu Val
610 615 620

Arg Thr Ala Arg Leu Leu Ser Glu Arg Asp Val Ala Lys His Arg Leu
625 630 635 640

Val Val Leu Val Lys Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala
645 650 655

Thr Leu Gln Val Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro
660 665 670

Leu Pro Glu Ala Ala Pro Ala Gln Ala Gln Ala Asp Ser Leu Thr Val
675 680 685

Tyr Leu Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser
690 695 700

Val Phe Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala
705 710 715 720

Ser Val Gly Arg Cys Ser Val Pro Glu Gly Pro Phe Pro Gly His Leu
725 730 735

Val Asp Val Ser Gly Thr Gly Thr Leu Ser Gln Ser Tyr Gln Tyr Glu
740 745 750

Val Cys Leu Thr Gly Gly Ser Glu Ser Asn Asp Phe Lys Phe Leu Lys
755 760 765

Pro Ile Phe Pro Asn Ile Val Ser Gln Asp Ser Arg Arg Lys Ser Glu
770 775 780

Phe Leu Glu
785

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 138..2528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GTGATTGGAC GTGTTTTGT GACTATTTGG GAAGAAAGACA CCTTCCTAAC CAGATTTACT 60
CCAATATCTT CCCGGACCCCT CATGAGTGGA TTGCAATTGA CTTGAAGAAG CAGCACCCCTC 120
AGGACTGAAT CTGAACCA ATG GAG ACA GCA CTA GCA AAA ATA CCA CAG CAA 170
Met Glu Thr Ala Leu Ala Lys Ile Pro Gln Gln
1 5 10

AGG CAA GTC TTT CTT ACT ATA TTG TCG TTA TTG TGG AAG TCT AGC Arg Gln Val Phe Phe Leu Thr Ile Leu Ser Leu Leu Trp Lys Ser Ser 15 20 25	218
TCT GAG GCC ATT AGA TAT TCC ATG CCA GAA GAA ACA GAG AGT GGC TAT Ser Glu Ala Ile Arg Tyr Ser Met Pro Glu Glu Thr Glu Ser Gly Tyr 30 35 40	266
ATG GTG GCT AAC CTG GCG AAA GAT CTG GGG ATC AGG GTT GGA GAA CTG Met Val Ala Asn Leu Ala Lys Asp Leu Gly Ile Arg Val Gly Glu Leu 45 50 55	314
TCC TCT AGA GGA GCT CAA ATC CAT TAC AAA GGA AAC AAA GAA CTT TTG Ser Ser Arg Gly Ala Gln Ile His Tyr Lys Gly Asn Lys Glu Leu Leu 60 65 70 75	362
CAG CTG GAT GCA GAG ACT GGG AAT TTG TTC TTA AAG GAA AAA CTA GAC Gln Leu Asp Ala Glu Thr Gly Asn Leu Phe Leu Lys Glu Lys Leu Asp 80 85 90	410
AGA GAA CTG CTG TGT GGA GAG ACA GAA CCC TGT GTG CTG AAC TTC CAG Arg Glu Leu Leu Cys Gly Glu Thr Glu Pro Cys Val Leu Asn Phe Gln 95 100 105	458
ATC ATA CTG GAA AAC CCT ATG CAG TTC TTC CAA ACT GAA CTG CAG CTC Ile Ile Leu Glu Asn Pro Met Gln Phe Phe Gln Thr Glu Leu Gln Leu 110 115 120	506
ACA GAT ATA AAC GAC CAT TCT CCA GAG TTC CCC AAC AAG AAA ATG CTT Thr Asp Ile Asn Asp His Ser Pro Glu Phe Pro Asn Lys Lys Met Leu 125 130 135	554
CTA ACA ATT CCT GAG AGT GCC CAT CCA GGG ACT GTG TTT CCT CTG AAG Leu Thr Ile Pro Glu Ser Ala His Pro Gly Thr Val Phe Pro Leu Lys 140 145 150 155	602
GCA GCT CGG GAC TCT GAC ATA GGG AGC AAC GCT GTT CAG AAC TAC ACA Ala Ala Arg Asp Ser Asp Ile Gly Ser Asn Ala Val Gln Asn Tyr Thr 160 165 170	650
GTC AAT CCC AAC CTC CAT TTC CAC GTC GTT ACT CAC AGT CGC ACA GAT Val Asn Pro Asn Leu His Phe His Val Val Thr His Ser Arg Thr Asp 175 180 185	698
GGC AGG AAA TAC CCA GAG CTG GTG CTG GAC AGA GCC CTG GAT AGG GAG Gly Arg Lys Tyr Pro Glu Leu Val Leu Asp Arg Ala Leu Asp Arg Glu 190 195 200	746
GAG CAG CCT GAG CTC ACT TTA ATC CTC ACT GCT CTG GAT GGT GGA GCT Glu Gln Pro Glu Leu Thr Leu Ile Leu Thr Ala Leu Asp Gly Gly Ala 205 210 215	794
CCT TCC AGG TCA GGA ACC ACC ACA GTT CAC ATA GAA GTT GTG GAC ATC Pro Ser Arg Ser Gly Thr Thr Val His Ile Glu Val Val Asp Ile 220 225 230 235	842
AAT GAT AAC TCC CCC CAG TTT GTA CAG TCA CTC TAT AAG GTG CAA GTT Asn Asp Asn Ser Pro Gln Phe Val Gln Ser Leu Tyr Lys Val Gln Val 240 245 250	890

CCT GAG AAT AAT CCC CTC AAT GCC TTT GTT GTC ACG GTC TCT GCC ACG Pro Glu Asn Asn Pro Leu Asn Ala Phe Val Val Thr Val Ser Ala Thr 255 260 265	938
GAT TTA GAT GCT GGG GTA TAT GGC AAT GTG ACC TAT TCT CTG TTT CAA Asp Leu Asp Ala Gly Val Tyr Gly Asn Val Thr Tyr Ser Leu Phe Gln 270 275 280	986
GGG TAT GGG GTA TTT CAA CCA TTT GTA ATA GAC GAA ATC ACT GGA GAA Gly Tyr Gly Val Phe Gln Pro Phe Val Ile Asp Glu Ile Thr Gly Glu 285 290 295	1034
ATC CAT CTG AGC AAA GAG CTG GAT TTT GAG GAA ATT AGC AAT CAT AAC Ile His Leu Ser Lys Glu Leu Asp Phe Glu Glu Ile Ser Asn His Asn 300 305 310 315	1082
ATA GAA ATC GCA GCC ACA GAT GGA GGA GGC CTT TCA GGA AAA TGC ACT Ile Glu Ile Ala Ala Thr Asp Gly Gly Leu Ser Gly Lys Cys Thr 320 325 330	1130
GTG GCT GTA CAG GTG TTG GAT GTG AAT GAC AAC GCC CCA GAG TTG ACA Val Ala Val Gln Val Leu Asp Val Asn Asp Asn Ala Pro Glu Leu Thr 335 340 345	1178
ATT AGG AAG CTC ACA GTC CTG GTC CCA GAA AAT TCC GCA GAG ACT GTA Ile Arg Lys Leu Thr Val Leu Val Pro Glu Asn Ser Ala Glu Thr Val 350 355 360	1226
GTT GCT GTT TTT AGT GTT TCT GAT TCT GAT TCG GGG GAC AAT GGA AGG Val Ala Val Phe Ser Val Ser Asp Ser Asp Ser Gly Asp Asn Gly Arg 365 370 375	1274
ATG GTG TGT TCT ATT CCG AAC AAT ATC CCA TTT CTC CTG AAA CCC ACA Met Val Cys Ser Ile Pro Asn Asn Ile Pro Phe Leu Leu Lys Pro Thr 380 385 390 395	1322
TTT GAG AAT TAT TAC ACG TTA GTG ACT GAG GGG CCA CTT GAT AGA GAG Phe Glu Asn Tyr Tyr Leu Val Thr Glu Gly Pro Leu Asp Arg Glu 400 405 410	1370
AAC AGA GCT GAG TAC AAC ATC ACC ATC ACG GTC TCA GAT CTG GGC ACA Asn Arg Ala Glu Tyr Asn Ile Thr Ile Thr Val Ser Asp Leu Gly Thr 415 420 425	1418
CCC AGG CTC ACA ACC CAG CAC ACC ATA ACA GTG CAA GTG TCC GAC ATC Pro Arg Leu Thr Thr Gln His Thr Ile Thr Val Gln Val Ser Asp Ile 430 435 440	1466
AAC GAC AAC GCC CCT GCC TTC ACC CAA ACC TCC TAC ACC ATG TTT GTC Asn Asp Asn Ala Pro Ala Phe Thr Gln Thr Ser Tyr Thr Met Phe Val 445 450 455	1514
CAC GAG AAC AAC AGC CCC GCC CTG CAC ATA GGC ACC ATC AGT GCC ACA His Glu Asn Asn Ser Pro Ala Leu His Ile Gly Thr Ile Ser Ala Thr 460 465 470 475	1562
GAC TCA GAC TCA GGC TCC AAT GCC CAC ATC ACC TAC TCG CTG CTG CCG Asp Ser Asp Ser Gly Ser Asn Ala His Ile Thr Tyr Ser Leu Leu Pro 480 485 490	1610

CCT GAT GAC CCG CAG CTG GCC CTC GAC TCA CTC ATC TCC ATC AAT GTT Pro Asp Asp Pro Gln Leu Ala Leu Asp Ser Leu Ile Ser Ile Asn Val 495 500 505	1658
GAC AAT GGG CAG CTG TTC GCG CTC AGA GCT CTA GAC TAT GAG GCA CTG Asp Asn Gly Gln Leu Phe Ala Leu Arg Ala Leu Asp Tyr Glu Ala Leu 510 515 520	1706
CAG TCC TTC GAG TTC TAC GTG GGC GCT ACA GAT GGA GGC TCA CCC GCG Gln Ser Phe Glu Phe Tyr Val Gly Ala Thr Asp Gly Gly Ser Pro Ala 525 530 535	1754
CTC AGC AGC CAG ACT CTG GTG CGG ATG GTG GTG CTG GAT GAC AAT GAC Leu Ser Ser Gln Thr Leu Val Arg Met Val Val Leu Asp Asp Asn Asp 540 545 550 555	1802
AAT GCC CCC TTC GTG CTC TAC CCA CTG CAG AAT GCC TCA GCA CCC TGT Asn Ala Pro Phe Val Leu Tyr Pro Leu Gln Asn Ala Ser Ala Pro Cys 560 565 570	1850
ACT GAG CTA CTG CCT AGG GCA GCA GAG CCC GGC TAC CTG ATC ACC AAA Thr Glu Leu Leu Pro Arg Ala Ala Glu Pro Gly Tyr Leu Ile Thr Lys 575 580 585	1898
GTG GTG GCT GTG GAT CGC GAC TCT GGA CAG AAT GCT TGG CTG TCG TTC Val Val Ala Val Asp Arg Asp Ser Gly Gln Asn Ala Trp Leu Ser Phe 590 595 600	1946
CAG CTA CTT AAA GCT ACA GAG CCA GGG CTG TTC AGT GTA TGG GCA CAC Gln Leu Leu Lys Ala Thr Glu Pro Gly Leu Phe Ser Val Trp Ala His 605 610 615	1994
AAT GGT GAA GTG CGC ACC ACT AGG CTG CTG AGT GAG CGA GAT GCT CAG Asn Gly Glu Val Arg Thr Thr Arg Leu Leu Ser Glu Arg Asp Ala Gln 620 625 630 635	2042
AAG CAC AAG CTA CTG CTG GTC AAG GAC AAT GGC GAT CCT CTG CGC Lys His Lys Leu Leu Leu Val Lys Asp Asn Gly Asp Pro Leu Arg 640 645 650	2090
TCT GCC AAT GTC ACT CTT CAC GTG CTA GTG GTG GAT GGC TTC TCG CAG Ser Ala Asn Val Thr Leu His Val Leu Val Val Asp Gly Phe Ser Gln 655 660 665	2138
CCT TAC CTA CCA TTG GCT GAG GTG GCA CAG GAT TCC ATG CAA GAT AAT Pro Tyr Leu Pro Leu Ala Glu Val Ala Gln Asp Ser Met Gln Asp Asn 670 675 680	2186
TAC GAC GTT CTC ACA CTG TAC CTA GTC ATT GCC TTG GCA TCT GTA TCT Tyr Asp Val Leu Thr Leu Tyr Leu Val Ile Ala Leu Ala Ser Val Ser 685 690 695	2234
TCT CTC TTC CTC TTG TCT GTA GTG CTG TTT GTG GGG GTG AGG CTG TGC Ser Leu Phe Leu Leu Ser Val Val Leu Phe Val Gly Val Arg Leu Cys 700 705 710 715	2282
AGG AGG GCC AGG GAG GCC TCC TTG GGT GAC TAC TCT GTG CCT GAG GGA Arg Arg Ala Arg Glu Ala Ser Leu Gly Asp Tyr Ser Val Pro Glu Gly 720 725 730	2330
CAC TTT CCT AGC CAC TTG GTG GAT GTC AGC GGT GCC GGG ACC CTG TCC	2378

His Phe Pro Ser His Leu Val Asp Val Ser Gly Ala Gly Thr Leu Ser		
735	740	745
CAG AGT TAT CAA TAT GAG GTG TGT CTT AAT GGA GGT ACT AGA ACA AAT		2426
Gln Ser Tyr Gln Tyr Glu Val Cys Leu Asn Gly Gly Thr Arg Thr Asn		
750	755	760
GAG TTT AAC TTT CTT AAA CCA TTG TTT CCT ATC CTT CCG ACC CAG GCT		2474
Glu Phe Asn Phe Leu Lys Pro Leu Phe Pro Ile Leu Pro Thr Gln Ala		
765	770	775
GCT GCT GCT GAA GAA AGA GAA AAC GCT GTT GTG CAC AAT AGC GTT GGA		2522
Ala Ala Ala Glu Glu Arg Glu Asn Ala Val Val His Asn Ser Val Gly		
780	785	790
TTC TAT TAGAGCACTG ATTTTGAAGT GGTGGTTACC TCATTTTCC TTAACTATCC		2578
Phe Tyr		
CTGATGTAGA ATGGTGTAGT GCCGTGAATC AACTCCTGAG ATATATGTTA ATTTTATCCT		2638
TTGTTTGAA TCAAACATT CAGATGTGAT CCTACTCTAG AGAATTGGT TCTACTCCAT		2698
TGTGTTGTT TAGATTTCTA CGCCATACCA GTGCATGCTG GGTTGTTTT TTTTTTACAA		2758
TTATTATAAC TTTGCTTGG AGGGGAACTC ATATTCGCTG TAACGAATTG GAACCACTTT		2818
CATTGTTAGA GATGCCTTGC TTTGTTGTGT TATTTCAGAC AGGGTCTTAA ATTGTAGCCC		2878
TGGGTGACCT GAAATGACTA TGTACAGACT GACTTTGAAT TTGTGGCAGT CCATCTGCCT		2938
CTGTTGTCCT ATGTTGGGAT TGTGAGCATG CATGAGTAGG CTCAGCTGTG GTGAGCGACC		2998
TTAATAAAAAA TCAAATACTA AAAAAAAAAA AAAAAA		3033

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met	Glu	Thr	Ala	Leu	Ala	Lys	Ile	Pro	Gln	Gln	Arg	Gln	Val	Phe	Phe
1				5					10				15		
Leu	Thr	Ile	Leu	Ser	Leu	Leu	Trp	Lys	Ser	Ser	Ser	Glu	Ala	Ile	Arg
					20			25				30			
Tyr	Ser	Met	Pro	Glu	Glu	Thr	Glu	Ser	Gly	Tyr	Met	Val	Ala	Asn	Leu
						35		40			45				
Ala	Lys	Asp	Leu	Gly	Ile	Arg	Val	Gly	Glu	Leu	Ser	Ser	Arg	Gly	Ala
					50		55			60					
Gln	Ile	His	Tyr	Lys	Gly	Asn	Lys	Glu	Leu	Leu	Gln	Leu	Asp	Ala	Glu
						65		70		75			80		

Thr Gly Asn Leu Phe Leu Lys Glu Lys Leu Asp Arg Glu Leu Leu Cys
85 90 95

Gly Glu Thr Glu Pro Cys Val Leu Asn Phe Gln Ile Ile Leu Glu Asn
100 105 110

Pro Met Gln Phe Phe Gln Thr Glu Leu Gln Leu Thr Asp Ile Asn Asp
115 120 125

His Ser Pro Glu Phe Pro Asn Lys Lys Met Leu Leu Thr Ile Pro Glu
130 135 140

Ser Ala His Pro Gly Thr Val Phe Pro Leu Lys Ala Ala Arg Asp Ser
145 150 155 160

Asp Ile Gly Ser Asn Ala Val Gln Asn Tyr Thr Val Asn Pro Asn Leu
165 170 175

His Phe His Val Val Thr His Ser Arg Thr Asp Gly Arg Lys Tyr Pro
180 185 190

Glu Leu Val Leu Asp Arg Ala Leu Asp Arg Glu Glu Gln Pro Glu Leu
195 200 205

Thr Leu Ile Leu Thr Ala Leu Asp Gly Gly Ala Pro Ser Arg Ser Gly
210 215 220

Thr Thr Thr Val His Ile Glu Val Val Asp Ile Asn Asp Asn Ser Pro
225 230 235 240

Gln Phe Val Gln Ser Leu Tyr Lys Val Gln Val Pro Glu Asn Asn Pro
245 250 255

Leu Asn Ala Phe Val Val Thr Val Ser Ala Thr Asp Leu Asp Ala Gly
260 265 270

Val Tyr Gly Asn Val Thr Tyr Ser Leu Phe Gln Gly Tyr Gly Val Phe
275 280 285

Gln Pro Phe Val Ile Asp Glu Ile Thr Gly Glu Ile His Leu Ser Lys
290 295 300

Glu Leu Asp Phe Glu Glu Ile Ser Asn His Asn Ile Glu Ile Ala Ala
305 310 315 320

Thr Asp Gly Gly Leu Ser Gly Lys Cys Thr Val Ala Val Gln Val
325 330 335

Leu Asp Val Asn Asp Asn Ala Pro Glu Leu Thr Ile Arg Lys Leu Thr
340 345 350

Val Leu Val Pro Glu Asn Ser Ala Glu Thr Val Val Ala Val Phe Ser
355 360 365

Val Ser Asp Ser Asp Ser Gly Asp Asn Gly Arg Met Val Cys Ser Ile
370 375 380

Pro Asn Asn Ile Pro Phe Leu Leu Lys Pro Thr Phe Glu Asn Tyr Tyr
385 390 395 400

Thr Leu Val Thr Glu Gly Pro Leu Asp Arg Glu Asn Arg Ala Glu Tyr
405 410 415

Asn Ile Thr Ile Thr Val Ser Asp Leu Gly Thr Pro Arg Leu Thr Thr
420 425 430

Gln His Thr Ile Thr Val Gln Val Ser Asp Ile Asn Asp Asn Ala Pro
435 440 445

Ala Phe Thr Gln Thr Ser Tyr Thr Met Phe Val His Glu Asn Asn Ser
450 455 460

Pro Ala Leu His Ile Gly Thr Ile Ser Ala Thr Asp Ser Asp Ser Gly
465 470 475 480

Ser Asn Ala His Ile Thr Tyr Ser Leu Leu Pro Pro Asp Asp Pro Gln
485 490 495

Leu Ala Leu Asp Ser Leu Ile Ser Ile Asn Val Asp Asn Gly Gln Leu
500 505 510

Phe Ala Leu Arg Ala Leu Asp Tyr Glu Ala Leu Gln Ser Phe Glu Phe
515 520 525

Tyr Val Gly Ala Thr Asp Gly Gly Ser Pro Ala Leu Ser Ser Gln Thr
530 535 540

Leu Val Arg Met Val Val Leu Asp Asp Asn Asp Asn Ala Pro Phe Val
545 550 555 560

Leu Tyr Pro Leu Gln Asn Ala Ser Ala Pro Cys Thr Glu Leu Leu Pro
565 570 575

Arg Ala Ala Glu Pro Gly Tyr Leu Ile Thr Lys Val Val Ala Val Asp
580 585 590

Arg Asp Ser Gly Gln Asn Ala Trp Leu Ser Phe Gln Leu Leu Lys Ala
595 600 605

Thr Glu Pro Gly Leu Phe Ser Val Trp Ala His Asn Gly Glu Val Arg
610 615 620

Thr Thr Arg Leu Leu Ser Glu Arg Asp Ala Gln Lys His Lys Leu Leu
625 630 635 640

Leu Leu Val Lys Asp Asn Gly Asp Pro Leu Arg Ser Ala Asn Val Thr
645 650 655

Leu His Val Leu Val Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu
660 665 670

Ala Glu Val Ala Gln Asp Ser Met Gln Asp Asn Tyr Asp Val Leu Thr
675 680 685

Leu Tyr Leu Val Ile Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Leu
690 695 700

Ser Val Val Leu Phe Val Gly Val Arg Leu Cys Arg Arg Ala Arg Glu
705 710 715 720

Ala Ser Leu Gly Asp Tyr Ser Val Pro Glu Gly His Phe Pro Ser His
725 730 735

Leu Val Asp Val Ser Gly Ala Gly Thr Leu Ser Gln Ser Tyr Gln Tyr
740 745 750

Glu Val Cys Leu Asn Gly Gly Thr Arg Thr Asn Glu Phe Asn Phe Leu
755 760 765

Lys Pro Leu Phe Pro Ile Leu Pro Thr Gln Ala Ala Ala Ala Glu Glu
770 775 780

Arg Glu Asn Ala Val Val His Asn Ser Val Gly Phe Tyr
785 790 795

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AAAACACGGG GGAAATGACA GTAGCAAAGA ATCTGGACTA TGAAGAACATGC TCATTGTATG	60
AAATGGAAAT ACAGGGCTGAA GATGTGGGG CGCTTCTGGG GAGGAGCAAA GTGGTAATTA	120
TGGTAGAAGA TGTAAATGAC AATCGGCCAG AAGTGACCAT TACATCCTTG TTTAACCCGG	180
TATTGGAAAA TTCTCTTCCC GGGACAGTAA TTGCCTTCCTT GAATGTGCAT GACCGAGACT	240
CTGGAAAGAA CGGCCAAGTT GTCTGTTACA CGCATGATAA CTTACCTTTT AAATTAGAAA	300
AGTCAATAGA TAATTATTAT AGATTGGTGA CATGGAAATA TTTGGACCGA GAAAAAGTCT	360
CCATCTACAA TATCACAGTG ATAGCCTCAG ATCTAGGAGC CCACTCTGTC ACTGAAACCT	420
ACATTGCCCT GATTGTGGCA GACACTAATG ACAACCCCTCC TCGTTTCTT CACACCTCCT	480
ACACAGCCTA TATTCCAGAG AACAAACCTGA GGGGCGCCTC CATCTTCTCA CTGACTGCAC	540
ATGATCCTGA CAGTCAGGAA AATGCACAGG TCACTTACTC TGTGTCTGAG GACACCATAAC	600
AGGGAGTGCC TTTGTCTCT TATATCTCCA TCAACTCAGA TACTGGTGTGTC CTGTATGCAC	660
TGCACTCTTT TGACTTCGAG AAGATACAAG ACTTGCAGCT ACTGGTTGTT GCCACTGACA	720
GTGGAAGCCC ACCTCTCAGC AGCAATGTGT CATTGAGCTT GTTGTGTTG GACCAGAACG	780
ACAAACGCACC TGAGATTCTA TATCCTAGCT TCCCCACAGA TGGCTCCACT GGTGTGGAAC	840
TAGCACCCCCG CTCTGCAGAG CCTGGATACC TAGTGACCAA AGTGGTGGCA GTGGACAAAG	900
ACTCAGGACA GAATGTTGG CTGTCCTACC GTCTGCTGAA GGCCAGCGAA CCTGGGCTCT	960
TCTCTGTAGG ACTTCACACG GGTGAGGTGC GTACAGCGAG GGCCCTGCTG GACAGAGATG	1020

CTCTCAAACA	GAATCTGGTG	ATGGCCGTGC	AGGACCATGG	CCAACCCCCT	CTCTCGGCCA	1080
CTGTAACTCT	CACTGTGGCA	GTGGCTAACCA	GCATCCCTGA	GGTGTGGCT	GACTTGAGCA	1140
GCATTAGGAC	CCCTGGGTA	CCAGAGGATT	CTGATATCAC	GCTCCACCTG	GTGGTGGCAG	1200
TGGCTGTGGT	CTCCTGTGTC	TTCCCTGTCT	TTGTCATTGT	CCTCCTAGCT	CTCAGGCTTC	1260
AGCGCTGGCA	GAAGTCTCGC	CAGCTCCAGG	GCTCCAAAGG	TGGATTGGCT	CCTGCACCTC	1320
CATCACATT	TGTGGGCATC	GACGGGGTAC	AGGCTTTCT	ACAAAACCTAT	TCTCATGAAG	1380
TCTCGCTCAC	TTCAGGCTCC	CAGACAAGCC	ACATTATCTT	TCCTCAGCCC	AACTATGCAG	1440
ACATGCTCAT	TAACCAAGAA	GGCTGTGAGA	AAAATGATTTC	CTTATTAACA	TCCATAGATT	1500
TTCATGAGAG	TAACCGTGAA	GATGCTTGCG	CCCCGCAAGC	CCCGCCCCAAC	ACTGACTGGC	1560
GTTCCTCTCA	AGCCCAGAGA	CCCGGCACGA	GC GGATCCC	AAATGGGGAT	GAAACCGGCA	1620
CCTGGCCCAA	CAACCAGTTC	GATACAGAGA	TGCTGCAAGC	CATGATCTTG	GCCTCTGCCA	1680
GTGAAGCCGC	TGATGGGAGC	TCCACTCTGG	GAGGGGGCAC	TGGCACTATG	GGTTTGAGCG	1740
CTCGATATGG	ACCCCAGTTT	ACCCCTGCAGC	ACGTGCCTGA	CTACCGCCAG	AACGTGTACA	1800
TCCCTGGCAG	CAATGCCACA	CTGACCAACG	CAGCTGGCAA	ACGAGATGGC	AAGGCTCCGG	1860
CAGGCGGCAA	TGGCAACAAC	AACAAGTCGG	GCAAGAAAGA	GAAGAAGTAA	TATGGAGGCC	1920
AGGCCTTGAG	CCACAGGGCA	GCCTCCCTCC	CCAGCCAGTC	CAGCTTGTC	TTACTTGTAC	1980
CCAGGCCTCA	GAATTTCAAGG	GTCACCCCCA	GGATTCTGGT	AGGAGCCACA	GCCAGGCCAT	2040
GCTCCCCGTT	GGGAAACAGA	AACAAGTGCC	CAAGCCAACA	CCCCCTCTTT	GTACCCTAGG	2100
GGGGTTGAAT	ATGCAAAGAG	AGTTCTGCTG	GGACCCCCTA	TCCAATCAGT	GATTGTACCC	2160
ACATAGGTAG	CAGGGTTAGT	GTGGATAACAC	ACACACACAC	ACACACACAC	ACACACACAA	2220
CCCTTGTCCCT	CCGCAGTGCC	TGCCACTTTC	TGGGACTTTTC	TCATCCCCCT	ACGCCCTTCC	2280
TTTATCCTCT	CCCACCCAGA	CACAGCTGCT	GGAGAATAAA	TTTGGGGATG	CTGATGCTAA	2340
AAAAAAA						2347

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

A GAG GCT GCT CAC CAC CTG GTC CTC ACG GCC TCG GAT GGC GGC AAG	46
Glu Ala Ala His His Leu Val Leu Thr Ala Ser Asp Gly Gly Lys	
1 5 10 15	
CCG CCT CGC TCT AGC ACA GTG CGC ATC CAC GTG ACA GTG TTG GAT ACA	94
Pro Pro Arg Ser Ser Thr Val Arg Ile His Val Thr Val Leu Asp Thr	
20 25 30	
AAT GAC AAT GCC CCG GTT TTT CCT CAC CCG ATT TAC CGA GTG AAA GTC	142
Asn Asp Asn Ala Pro Val Phe Pro His Pro Ile Tyr Arg Val Lys Val	
35 40 45	
CTT GAG AAC ATG CCC CCA GGC ACG CGG CTG CTT ACT GTA ACA GCC AGC	190
Leu Glu Asn Met Pro Pro Gly Thr Arg Leu Leu Thr Val Thr Ala Ser	
50 55 60	
GAC CCG GAT GAG GGA ATC AAC GGA AAA GTG GCA TAC AAA TTC CGG AAA	238
Asp Pro Asp Glu Gly Ile Asn Gly Lys Val Ala Tyr Lys Phe Arg Lys	
65 70 75	
ATT AAT GAA AAA CAA ACT CCG TTA TTC CAG CTT AAT GAA AAT ACT GGG	286
Ile Asn Glu Lys Gln Thr Pro Leu Phe Gln Leu Asn Glu Asn Thr Gly	
80 85 90 95	
GAA ATA TCA ATA GCA AAA AGT CTA GAT TAT GAA GAA TGT TCA TTT TAT	334
Glu Ile Ser Ile Ala Lys Ser Leu Asp Tyr Glu Glu Cys Ser Phe Tyr	
100 105 110	
GAA ATG GAA ATA CAA GCC GAA GAT GTG GGG GCA CTT CTG GGG AGG ACC	382
Glu Met Glu Ile Gln Ala Glu Asp Val Gly Ala Leu Leu Gly Arg Thr	
115 120 125	
AAA TTG CTC ATT TCT GTG GAA GAT GTA AAT GAC AAT AGA CCA GAA GTG	430
Lys Leu Leu Ile Ser Val Glu Asp Val Asn Asp Asn Arg Pro Glu Val	
130 135 140	
ATC ATT ACG TCT TTG TTT AGC CCA GTG TTA GAA AAT TCT CTT CCC GGG	478
Ile Ile Thr Ser Leu Phe Ser Pro Val Leu Glu Asn Ser Leu Pro Gly	
145 150 155	
ACA GTA ATT GCC TTC TTG AGT GTG CAT GAC CAA GAC TCT GGA AAG AAT	526
Thr Val Ile Ala Phe Leu Ser Val His Asp Gln Asp Ser Gly Lys Asn	
160 165 170 175	
GGT CAA GTT GTC TGT TAC ACA CGT GAT AAT TTA CCT TTT AAA TTA GAA	574
Gly Gln Val Val Cys Tyr Thr Arg Asp Asn Leu Pro Phe Lys Leu Glu	
180 185 190	
AAG TCA ATA GGT AAT TAT TAT AGA TTA GTG ACA AGG AAA TAT TTG GAC	622
Lys Ser Ile Gly Asn Tyr Tyr Arg Leu Val Thr Arg Lys Tyr Leu Asp	
195 200 205	
CGA GAA AAT GTC TCT ATC TAC AAT ATC ACA GTG ATG GCC TCA GAT CTA	670
Arg Glu Asn Val Ser Ile Tyr Asn Ile Thr Val Met Ala Ser Asp Leu	
210 215 220	
GGA ACA CCA CCT CTG TCC ACT GAA ACT CAA ATC GCT CTG CAC GTG GCA	718
Gly Thr Pro Pro Leu Ser Thr Glu Thr Gln Ile Ala Leu His Val Ala	
225 230 235	

GAC ATT AAC GAC AAC CCT CCT ACT TTC CCT CAT GCC TCC TAC TCA GCG Asp Ile Asn Asp Asn Pro Pro Thr Phe Pro His Ala Ser Tyr Ser Ala	766
240 245 250 255	
TAT ATC CTA GAG AAC AAC CTG AGA GGA GCC TCC ATC TTT TCC TTG ACT Tyr Ile Leu Glu Asn Asn Leu Arg Gly Ala Ser Ile Phe Ser Leu Thr	814
260 265 270	
GCA CAC GAC CCC GAC AGC CAG GAG AAT GCC CAG GTC ACT TAC TCT GTG Ala His Asp Pro Asp Ser Gln Glu Asn Ala Gln Val Thr Tyr Ser Val	862
275 280 285	
ACC GAG GAC ACG CTG CAG GGG GCG CCC CTG TCC TCG TAT ATC TCC ATC Thr Glu Asp Thr Leu Gln Gly Ala Pro Leu Ser Ser Tyr Ile Ser Ile	910
290 295 300	
AAC TCT GAC ACC GGT GTC CTG TAT GCG CTG CAA TCT TTC GAC TAT GAG Asn Ser Asp Thr Gly Val Leu Tyr Ala Leu Gln Ser Phe Asp Tyr Glu	958
305 310 315	
CAG ATC CGA GAC CTG CAG CTA CTG GTA ACA GCC AGC GAC AGC GGG GAC Gln Ile Arg Asp Leu Gln Leu Leu Val Thr Ala Ser Asp Ser Gly Asp	1006
320 325 330 335	
CCG CCC CTC AGC AGC AAC ATG TCA CTG AGC CTG TTC GTG CTG GAC CAG Pro Pro Leu Ser Ser Asn Met Ser Leu Ser Leu Phe Val Leu Asp Gln	1054
340 345 350	
AAT GAC AAC GCG CCC GAG ATC CTG TAC CCC GCC CTC CCC ACA GAC GGT Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp Gly	1102
355 360 365	
TCC ACT GGC GTG GAG CTG GCG CCC CGC TCC GCA GAG CGT GGC TAC CTG Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Arg Gly Tyr Leu	1150
370 375 380	
G TG ACC AAG GTG GTG GCG GTG GAC AGA GAC TCG GGC CAG AAC GCC TGG Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln Asn Ala Trp	1198
385 390 395	
CTG TCC TAC CGC CTG CTC AAG GCC AGC GAG CCG GGA CTC TTC TCG GTG Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly Leu Phe Ser Val	1246
400 405 410 415	
GGT CTG CAC ACG GGC GAG GTG CGC ACG GCG CGA GCC CTG CTG GAC AGA Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg Ala Leu Leu Asp Arg	1294
420 425 430	
GAC GCG CTC AAG CAG AGC CTC GTG GTG GCC GTC CAG GAC CAT GGC CAG Asp Ala Leu Lys Gln Ser Leu Val Val Ala Val Gln Asp His Gly Gln	1342
435 440 445	
CCC CCT CTC TCC GCC ACT GTC ACG CTC ACC GTA GCC GTG GCT GAC AGC Pro Pro Leu Ser Ala Thr Val Thr Leu Thr Val Ala Val Ala Asp Ser	1390
450 455 460	
ATC CCC GAA GTC CTG ACC GAG TTG GGC AGT CTG AAG CCT TCG GTC GAC Ile Pro Glu Val Leu Thr Glu Leu Gly Ser Leu Lys Pro Ser Val Asp	1438
465 470 475	

CCG AAC GAT TCG AGC CTT ACA CTC TAT CTC GTG GTG GCA GTG GCT GCC Pro Asn Asp Ser Ser Leu Thr Leu Tyr Leu Val Val Ala Val Ala Ala 480 485 490 495	1486
ATC TCC TGT GTC TTC CTC GCC TTT GTC GCT GTG CTT CTG GGG CTC AGG Ile Ser Cys Val Phe Leu Ala Phe Val Ala Val Leu Leu Gly Leu Arg 500 505 510	1534
CTG AGG CGC TGG CAC AAG TCA CGC CTG CTC CAG GAT TCC GGT GGC AGA Leu Arg Arg Trp His Lys Ser Arg Leu Leu Gln Asp Ser Gly Gly Arg 515 520 525	1582
TTG GTA GGC GTG CCT GCC TCA CAT TTT GTG GGT GTT GAG GAG GTA CAG Leu Val Gly Val Pro Ala Ser His Phe Val Gly Val Glu Glu Val Gln 530 535 540	1630
GCT TTC CTG CAG ACC TAT TCC CAG GAA GTC TCC CTC ACC GCC GAC TCG Ala Phe Leu Gln Thr Tyr Ser Gln Glu Val Ser Leu Thr Ala Asp Ser 545 550 555	1678
CGG AAG AGT CAC CTG ATC TTT CCC CAG CCC AAC TAC GCA GAC ATG CTC Arg Lys Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu 560 565 570 575	1726
ATC AGT CAG GAG GGC TGT GAG AAA AAT GAT TCT TTG TTA ACA TCC GTA Ile Ser Gln Glu Gly Cys Glu Lys Asn Asp Ser Leu Leu Thr Ser Val 580 585 590	1774
GAT TTT CAT GAA TAT AAG AAT GAA GCT GAT CAT GGT CAG GTG AGT TTA Asp Phe His Glu Tyr Lys Asn Glu Ala Asp His Gly Gln Val Ser Leu 595 600 605	1822
GTT CTT TGC TTG CTT TTA ATT TCC AGA TGAATTTAT TTGGCATAAAA Val Leu Cys Leu Leu Ile Ser Arg 610 615	1869
TTATGTTTG AAAAACATTG TGAAGATAGT TGAAAATAAT TTTTAAGGTG TATCACAGAG TTTTGGGTTT ATTTGGTGG TGTTACCAA AAATTGAACT CTAATAGTCA TAGGTTATTG	1929
TTTCATTTGC TTTTAAACGA CTTGGAAAAG ATTGTTCCAC CATTAAAC CTTCCAGTAT TTTATTCCTA TTATCACTCA TTCACTTAAG AAGTAGCTAC CCGTCCATAC TGGTAATTT	1989
GCTATTGTTT GTTTGTGTGT GTGTGTGTGT GTGTGTGTAT CCCAAACTAG AACTTCAGAA AATTATCAAG AAGTCTAAAG CCTTGTATT AGCTTAGCAA AAGTAAAATA	2049
TATCTCAGAA TTTTGTGGT TATGTTAGC ATTGAAACCT GTAAGTAGGC TCTTGTATAT TTCTTCACCT TAAACCTCTT TTCTGAGCCC TGTTCTGTA CCAGTGCCT TCAAAACTTT	2109
AATACTTCTT ACCATCCTTC AAAACATGAA CAAACTTAA AGATGGATCT TGGTGGGAGA TGAGACTGGT TACTAAATAT TAAGTATGTG AGTCAGTGGT CACCTGGGCT CCATCCCCAT	2169
GGAGACATGA AATCTAAAGC CTAGAATGTC CATTGCTCCC CCAAACAAAA AACAAAAGCA AAAACATTAG ATCTGAATTAA AAATGTAATT TTAAACTGTT GAAAGTGACT TTTGTAAAAT	2229
ATGTAAGAAC ATATTTCAAT ACAATTCCAA TTAGCTGTTT CGGTTGTGCA TTGATGTGAA	2589
	2649

GTGGTGAGAA TGTTGATATT AAGAACCAAT GTTTCAGGTA CACAAGTTCT AAATAAGCTG	2709
ATCAATTCAA TTAAAGTTAT TCAGTCTTGG CTGGACACAG TGCCTCATGT CTGAAATCCC	2769
AGCACTTTGG GAGGCTGGGG CAGGAGGACC GCTTGAGCCC CGGGGGTTTG AACTGCAGT	2829
GAGCTATGAT CATGCCACTG CACTCCAGCC TAGGTGGCAG AACTAGACCC TGTCTCTAAA	2889
AAAACATATTA TTAGGCCGCG TGCGGTGGCT CACGCCTGTA ATCCCAGCAC TTTGGGAGAC	2949
TGAGGTGGGT GGATCACCTG AGC	2972

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Glu Ala Ala His His Leu Val Leu Thr Ala Ser Asp Gly Gly Lys Pro
1 5 10 15

Pro Arg Ser Ser Thr Val Arg Ile His Val Thr Val Leu Asp Thr Asn
20 25 30

Asp Asn Ala Pro Val Phe Pro His Pro Ile Tyr Arg Val Lys Val Leu
35 40 45

Glu Asn Met Pro Pro Gly Thr Arg Leu Leu Thr Val Thr Ala Ser Asp
50 55 60

Pro Asp Glu Gly Ile Asn Gly Lys Val Ala Tyr Lys Phe Arg Lys Ile
65 70 75 80

Asn Glu Lys Gln Thr Pro Leu Phe Gln Leu Asn Glu Asn Thr Gly Glu
85 90 95

Ile Ser Ile Ala Lys Ser Leu Asp Tyr Glu Glu Cys Ser Phe Tyr Glu
100 105 110

Met Glu Ile Gln Ala Glu Asp Val Gly Ala Leu Leu Gly Arg Thr Lys
115 120 125

Leu Leu Ile Ser Val Glu Asp Val Asn Asp Asn Arg Pro Glu Val Ile
130 135 140

Ile Thr Ser Leu Phe Ser Pro Val Leu Glu Asn Ser Leu Pro Gly Thr
145 150 155 160

Val Ile Ala Phe Leu Ser Val His Asp Gln Asp Ser Gly Lys Asn Gly
165 170 175

Gln Val Val Cys Tyr Thr Arg Asp Asn Leu Pro Phe Lys Leu Glu Lys
180 185 190

Ser Ile Gly Asn Tyr Tyr Arg Leu Val Thr Arg Lys Tyr Leu Asp Arg
195 200 205

Glu Asn Val Ser Ile Tyr Asn Ile Thr Val Met Ala Ser Asp Leu Gly
210 215 220

Thr Pro Pro Leu Ser Thr Glu Thr Gln Ile Ala Leu His Val Ala Asp
225 230 235 240

Ile Asn Asp Asn Pro Pro Thr Phe Pro His Ala Ser Tyr Ser Ala Tyr
245 250 255

Ile Leu Glu Asn Asn Leu Arg Gly Ala Ser Ile Phe Ser Leu Thr Ala
260 265 270

His Asp Pro Asp Ser Gln Glu Asn Ala Gln Val Thr Tyr Ser Val Thr
275 280 285

Glu Asp Thr Leu Gln Gly Ala Pro Leu Ser Ser Tyr Ile Ser Ile Asn
290 295 300

Ser Asp Thr Gly Val Leu Tyr Ala Leu Gln Ser Phe Asp Tyr Glu Gln
305 310 315 320

Ile Arg Asp Leu Gln Leu Leu Val Thr Ala Ser Asp Ser Gly Asp Pro
325 330 335

Pro Leu Ser Ser Asn Met Ser Leu Ser Leu Phe Val Leu Asp Gln Asn
340 345 350

Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp Gly Ser
355 360 365

Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Arg Gly Tyr Leu Val
370 375 380

Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln Asn Ala Trp Leu
385 390 395 400

Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly Leu Phe Ser Val Gly
405 410 415

Leu His Thr Gly Glu Val Arg Thr Ala Arg Ala Leu Leu Asp Arg Asp
420 425 430

Ala Leu Lys Gln Ser Leu Val Val Ala Val Gln Asp His Gly Gln Pro
435 440 445

Pro Leu Ser Ala Thr Val Thr Leu Thr Val Ala Val Ala Asp Ser Ile
450 455 460

Pro Glu Val Leu Thr Glu Leu Gly Ser Leu Lys Pro Ser Val Asp Pro
465 470 475 480

Asn Asp Ser Ser Leu Thr Leu Tyr Leu Val Val Ala Val Ala Ala Ile
485 490 495

Ser Cys Val Phe Leu Ala Phe Val Ala Val Leu Leu Gly Leu Arg Leu
500 505 510

Arg Arg Trp His Lys Ser Arg Leu Leu Gln Asp Ser Gly Gly Arg Leu
515 520 525

Val Gly Val Pro Ala Ser His Phe Val Gly Val Glu Glu Val Gln Ala
530 535 540

Phe Leu Gln Thr Tyr Ser Gln Glu Val Ser Leu Thr Ala Asp Ser Arg
545 550 555 560

Lys Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Ile
565 570 575

Ser Gln Glu Gly Cys Glu Lys Asn Asp Ser Leu Leu Thr Ser Val Asp
580 585 590

Phe His Glu Tyr Lys Asn Glu Ala Asp His Gly Gln Val Ser Leu Val
595 600 605

Leu Cys Leu Leu Leu Ile Ser Arg
610 615

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MAY 10 2004

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MAY 10 2004

I hereby certify that this correspondence is being deposited with the U.S. Postal Service with sufficient postage as First Class Mail, in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on the date shown below.

Dated: 5-7-04

Signature:

Katherine L. Neville
Katherine L. Neville, Ph.D.

Docket No.: 27866/37501
(PATENT)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Suzuki, S.

Application No.: 09/880,573

Group Art Unit: 1647

Filed: June 13, 2001

Examiner: David Romeo

For: Protocadherin Materials and Methods

STATEMENT UNDER 37 C.F.R. §1.821

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted herewith in accordance with 37 C.F.R. §§1.821 and 1.825, are the same and include no new matter.

May 7, 2004

Respectfully submitted,

MARSHALL, GERSTEIN & BORUN LLP
6300 Sears Tower
233 South Wacker Drive
Chicago, Illinois 60606-6357
(312) 474-6300

By: *Katherine L. Neville*
Katherine L. Neville, Ph.D.
Reg. No. 53,379
Agent for Applicants



PC43	EC 1	(29)	ASTVIHYEIPPEERK-----GFAVGNVVANL--GLDLGSLSA--	(63)
	EC 2	(136)	PTQEMKLEISEAVAL-----GTRFPLESAH---DPDLGSNSL--	(169)
	EC 3	(245)	NQSLYRARVPGGCTS-----GTRVQVLAT---DLDEGPNGE--	(278)
	EC 4	(353)	GTVIALLSVT---DLDAGENGL--	(385)
	EC 5	(457)	SQSSYDVYIEENNLP-----GAPILNLSSW---DPDAPQNAR--	(490)
	EC 6	(567)	LYPRPGSSSVEMLPRGTS A-GHLVSRVWGW---DADAGHNAW--	(604)
PC42	EC 1	(42)	VPEEQPPNTLI-----GSL-----AADYGFDPDVG-	(65)
	EC 2	(147)	ASPVITLAIPENTNI-----GSLFPPIPLAS---DRDAGPNGV--	(180)
	EC 3	(247)	ERPSYEAEELSENSPI-----GHSVIVQVKAN---DSDDQGANAE--	(280)
	EC 4	(354)	EIRGIGLVTHQDGMANISEDVAEETAVALVQVSDRDEGENAA--	(395)
	EC 5	(473)	TQSVTEAFTPENNKP-----GEVIAETAS---DADSGNAE--	(506)
	EC 6	(579)	MLSGYNFSVMENMPA-----LSPVGMVTVI---DGDKGENAQ--	(612)
	EC 7	(682)	TAPSNTSHKLTPQTRL---GETVSQVAAE---DFDSGVNAE--	(717)
FAT	EC18	(1)	EDTVYSFDIPEWAQR-----GYQVGQIVAR---DADLGONAQ--	(34)
N-CAD	EC 1	(1)	DWVIPPINLPENSRG-----PFHQELVRIRS---DRDKNLSLRYT	(37)
	EC 2	(109)	LHQVWNGSVPPEGSKP-----GTYVMTVTAI---DADDPNALNGM	(144)
	EC 3	(224)	TAMTFYGEVPERVD-----IVANLTVT---DKDQPHTPAWN	(258)
	EC 4	(339)	APNPKITRQEGLHA---GTMLLTTFTAG---DPDRYMQQN--	(372)
	EC 5	(447)	LPQEAETCETPDPNNSINITAL-----DYDIDPNAGP-	(478)

MOTIF

..*0***v*EN***v-----Gr*v***v*A*---D*D*G*N***-

FIGURE 1A



PC43	EC 1	(64)	RRFPVSGASRR-----FFEVNRET-----GEMFVNDR-----	(91)
	EC 2	(170)	QTYELSRNEY-----FALRVQTREDSKYAELVLERA-----	(201)
	EC 3	(279)	IIYSFGSHNRAGVRQL--FALDLVT----GMLTIKGRL---	(309)
	EC 4	(386)	VTCVEVPPGLP-----FSLTSSLKNYFTLKTSA-----	(413)
	EC 5	(491)	LSEFFLLEQGAETGLVGRYFTINRDW-----GIVSSLLVP-----	(523)
	EC 6	(605)	LSYSLFGSPNOSL-----FAIGLHT----GOISTARPV-----	(633)
PC42	EC 1	(66)	HLYKLEVGAPE-----YLRVDGKT-----GDIIFTTETS-----	(92)
	EC 2	(181)	ASYELQVAED-----QEEKOPOLIVMGN-----	(203)
	EC 3	(281)	IEYTFHQAPEVVRRL---LRLDRNT---GLITVQGP-----	(310)
	EC 4	(396)	VTCWVAGDVP-----FQLRQAESTGSDSKKKYFLQTTTP	(429)
	EC 5	(507)	LWYSLEPEPAKGL---FTISPET-----GEIQVKTS-----	(535)
	EC 6	(613)	YOLSVEDNGD-----FVIQNGT-----GTILSSLS-----	(638)
	EC 7	(718)	LIYSAIGGNPYGL-----FOIGSHS-----GAITLEKE-----	(745)
FAT	EC18	(35)	LSYGWVSDWANDV-----FSLNPQT-----GMILTAR-----	(62)
N-CAD	EC 1	(38)	VTGPGADQPPPTGI-----FIINPIS-----GQLSVTKP-----	(65)
	EC 2	(145)	LRYRILSOAPSTPSPNW-FTINNET-----GDIITVAAG-----	(177)
	EC 3	(259)	AVTRISGGDPTGR-----FAIQTDPNSND-GLVTVVKP-----	(290)
	EC 4	(373)	IRYTKLSDPAN-----WLKIDPVN-----GQITTIAV-----	(399)
	EC 5	(479)	FAIDLPLSPVTIKRN--WTITRLN-----GDFAQNLK-----	(509)

MOTIF

I*0*I*****0*I***T-----G*I*T***T-----

FIGURE 1B



PC43	EC 1	(92)	LDREELCGTLPSCVTLELVENP-----	-LELFSEVVVIODINDNNPAF (135)
	EC 2	(202)	LDREREPSLQLVLTALDGGTPAL--	-SASLPIHIKVLDANDNAPVF (244)
	EC 3	(310)	LDFEDTKLHEITYIOAKDKGANPE--	-GAHCKVLVEVVVDVNDNAPEI (352)
	EC 4	(414)	LDRETYPEYNILSITARDAGTPSL--	-SALTIVRVQVSIDNDNPPQS (456)
	EC 5	(524)	LDYEDRREFELTAHISDGGBTPL--	-ATNISVNIFVFTDRNDNAPOV (566)
	EC 6	(634)	QDTDSRQTLTTL-IKDNGEPLSTTATLTVSVTEDSPEARAEFPSGSAPREQKKN (688)	
PC42	EC 1	(93)	IDREGLRECONQLPGDPCILEFEVSITDLVQNAS--	-PRLLEGOIEVODINDNTPNF (146)
	EC 2	(204)	LDRERWDSYDLTIKVQDGGSPPR--	-ATSALLRRTVLDTNNDNAPKF (246)
	EC 3	(311)	VDREDLSTLRFSSVLAKDQRGTNPK--	-SARAQWVVTVKDMNDNAPTI (353)
	EC 4	(430)	LDYEKVKDYTTEIVAVDSGNPPPL--	-SSTNSLKVQWVVDVNDNAPVF (472)
	EC 5	(536)	LDREQRESYELKVAADRGSPSL--	-QGTATATVLYNVLDCNNDPKF (578)
	EC 6	(639)	FDREQQSTYTFFQLKAVIDGGVPPR--	-SAYVGVTINVLDENDNAPYI (681)
	EC 7	(746)	IERRXHGLRVVKVSDRGKPPRYGTAHVHLVYNETLANRTLLETLLGHSLDTPLD (801)	(801) (802) IDIAGDPEYERSKORGN (818)
	FAT	EC18	(63)	LDYEEVOHYILLIVOAOODNGQPSL-----
N-CAD	EC 1	(66)	LDTITITYCNYVLNDNAPIF (105)	-STTITITYCNYVLNDNAPIF (105)
	EC 2	(178)	LDREQIARFHRAHDINGNOV--	-ENPIDIVINVIDMNNDNRPEF (108)
	EC 3	(291)	LDREKVKQYVTLITTOATDMEGNPTYGL-----	-SNTATAVITYTDVNDNPPEF (223)
	EC 4	(400)	IDFETNRMFVLTVAEENQVPLAKGIQHPP-----	-OSTATVSVTVIDVNE-NPYF (338)
	EC 5	(510)	LDRESPNVKNNIYNATFLASDNGIPPM-----	-SGTGTLQIYLLDINDNAPQV (446)
			IKFLEAGIYEVPIIIITDSGNPPKSNIKS-----	-ILRVRVRCQCDFTNGDCTDVDR (557)

MOTIF

LDRE*****0*L*V*A*D*G*P*-----
**T+TV*v*V*D*NDNAP*F

FIGURE 1C